



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 5 : C12Q 1/02, G01N 33/68	A1	(11) International Publication Number: WO 93/05172 (43) International Publication Date: 18 March 1993 (18.03.93)
(21) International Application Number: PCT/US92/07359 (22) International Filing Date: 28 August 1992 (28.08.92) (30) Priority data: 752,861 30 August 1991 (30.08.91) US (71) Applicant: CREATIVE BIOMOLECULES, INC. [US/US]; 35 South Street, Hopkinton, MA 01748 (US). (72) Inventors: SMART, John, E. ; 50 Meadow Brook Road, Weston, MA 02193 (US). OPPERMANN, Hermann ; 25 Summer Hill Road, Medway, MA 02053 (US). OZKAY-NAK, Engin ; 44 Purdue Drive, Milford, MA 01757 (US). KUBERASAMPATH, Thangavel ; 6 Spring Street, Medway, MA 02053 (US). RUEGER, David, C. ; 19 Downey Street, Hopkinton, MA 01748 (US). PANG, Roy, H., L. ; 15 Partridge Road, Etna, NH 03750 (US). COHEN, Charles, N. ; 98 Wintrop Street, Medway, MA 02053 (US).		(74) Agent: KELLEY, Robin, D.; Testa, Hurwitz & Thibault, 53 State Street/Exchange Place, Boston, MA 02018-2809 (US). (81) Designated States: AU, CA, JP, European patent (AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, SE). Published <i>With international search report. Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>
(54) Title: MORPHOGENIC PROTEIN SCREENING METHOD (57) Abstract Disclosed is a method of screening candidate compounds for the ability to modulate the level of morphogenic protein in mammalian system. The method includes determining a parameter indicative of the level of production of a morphogenic in a cell culture known to produce the morphogen, incubating a candidate compound with the culture for a time sufficient to allow the compound to affect the production of the morphogenic protein, and then assaying the culture again to detect a change in the level of morphogenic protein production.		

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MORPHOGENIC PROTEIN SCREENING METHOD

The invention relates to a method of screening drugs for the ability to modulate the level in mammals of proteins which can induce tissue morphogenesis and to methods of determining which animal tissue(s) and/or cell types within a tissue express a particular morphogenic protein.

Background of the Invention

Cell differentiation is the central characteristic of morphogenesis which initiates in the embryo, and continues to various degrees throughout the life of an organism in adult tissue repair and regeneration mechanisms. Members of the TGF- β superfamily include subfamilies of highly-related genes that now are suspected to play important roles in cell differentiation and morphogenesis during development and/or during adult life. For example, the *Drosophila* decapentaplegic gene product (DPP) has been implicated in formation of the dorsal-ventral axis in fruit flies; activins induce mesoderm and anterior structure formation in mammals; Müllerian inhibiting substance (MIS) may be required for male sex development in mammals; growth/differentiation factor-1 (GDF-1) has been implicated in nerve development and maintenance; other morphogenic proteins (BMP-2, -3, -4 and OP-1) induce bone formation.

The development and study of a bone induction model system has identified the developmental cascade of bone differentiation as consisting of chemotaxis of mesenchymal cells, proliferation of these progenitor cells, differentiation of cartilage, ossification and hypertrophy of this cartilaginous tissue, vascular invasion, bone formation, remodeling, and finally, marrow differentiation (Reddi (1981) Collagen Rel. Res. 1:209-206). This bone model system, which is studied in adult mammals, recapitulates the cascade of bone differentiation events that occur in formation of bone in the developing fetus. In other studies, the epithelium of the urinary bladder has been shown to induce new bone formation. Huggins (1931, Arch. Surg. 22:377-408) showed that new bone formation could be induced by surgical transplantation of urinary bladder epithelium onto the parietal fascia. Urist (1965, Science 150:893-899) demonstrated that implantation of demineralized bone segments resulted in endochondral bone formation. The latter study and observation suggested the existence of an osteogenic protein and that bovine diaphyseal bone was a source of enriched preparations of osteogenic protein (Sampath et al., J. Biol. Chem. 265:13198-13205, 1990; Urist, *ibid*; Reddi et al., Proc. Nat. Aca. Sci. 69:1601-1605, 1972; Sampath et al., Proc. Natl. Acad. Sci. 80:6591-6595, 1983). Proteins capable of inducing endochondral bone formation in mammals when implanted in association with a matrix now have been identified in a number of different mammalian species, as have the genes encoding these proteins, (see, for example, U.S. Patent No. 4,968,590; U.S.S.N. 315,342 filed February 23, 1989;

and U.S.S.N. 599,543, filed October 18, 1990). Human OP-1 DNA has been cloned from various cDNA and genomic libraries using a consensus probe (Ozkaynak et al., EMBO J. 9:2085-2093, 1990). Purified human recombinant OP-1, expressed in mammalian cells, has been shown to induce new bone formation in vivo. Like other members of the TGF- β superfamily, OP-1 is produced as a precursor, glycosylated, processed and secreted as a mature dimer. Mature OP-1 is cleaved at a maturation site following a sequence with the pattern of RXXR (Panganiban et al., Mol. Cell. Biol. 10:2669-2677, 1990).

The degree of morphogenesis in adult tissue varies among different tissues and depends on, among other factors, the degree of cell turnover in a given tissue. On this basis, tissues can be divided into three broad categories: 1) tissues with static cell populations such as nerve and skeletal muscle where there is little or no cell division and most of the cells formed during development persist throughout adult life and, therefore, possess little or no ability for normal regeneration after injury; 2) tissues containing conditionally renewing populations such as liver where there is generally little cell division but, in response to an appropriate stimulus or injury, cells can divide to produce daughters of the same differentiated cell type; and 3) tissues with permanently renewing populations including blood, bone, testes, and stratified squamous epithelia which are characterized by rapid and continuous cell turnover in the adult. Here, the terminally differentiated cells have a short life span and are replaced through

proliferation of a distinct subpopulation of cells, known as stem or progenitor cells.

It is an object of this invention to provide a method of screening compounds which, when administered to a given tissue from a given organism, cause an alteration in the level of morphogenic protein ("morphogen") produced by the tissue. Such compounds, when administered systemically, will result in altered systemic or local levels of morphogenic activity. This morphogenic activity includes the ability to induce proliferation and sequential differentiation of progenitor cells, and the ability to support and maintain the differentiated phenotype or sequence of phenotypes through the progression of events that results in the formation of normal adult tissue (including organ regeneration). Thus, broadly, the invention provides a key to development of additional modalities of therapies involving modulation of morphogenic protein production in animals or adult mammals, e.g., humans, and consequent correction of conditions involving pathologic alteration of the balance of tissue cell turnover. Another object of the invention is to provide methodologies for identifying or selecting a combination of compound(s) which may increase a progenitor cell population in a mammal, stimulate progenitor cells to differentiate in vivo or in vitro, maintain the differentiated phenotype or sequence of phenotypes of a tissue, induce tissue-specific growth in vivo, or replace diseased or damaged tissues or organs in vivo. Another object of the invention is to determine the tissue(s) or organ(s) of origin of a given morphogen. Another object of the

invention is to determine the specific cell type(s) within the tissue(s) or organ(s) of origin, or cell line(s) derived from the tissue(s), or organ(s) of origin, that is responsible for the synthesis and production of a given morphogen. These and other objects and features of the invention will be apparent from the description, drawing, and claims which follow.

Summary of the Invention

The invention features a method of screening candidate compounds for the ability to modulate the effective local or systemic concentration or level of morphogenic protein in an organism. The method is practiced by incubating one or more candidate compound(s) with cells from a test tissue type of an organism known to produce a given morphogen for a time sufficient to allow the compound(s) to affect the production, i.e., expression and/or secretion, of morphogen by the cells; and then assaying cells and the medium conditioned by the cells for a change in a parameter indicative of the level of production of the morphogenic protein. The procedure may be used to identify compounds showing promise as drugs for human use capable of increasing or decreasing morphogen production in vivo, thereby to correct or alleviate a diseased condition.

In a related aspect, the invention features a method of screening tissue(s) of an organism to assess whether or at what level cells of the tissue(s) produce a particular morphogen, thereby to determine a tissue(s) of origin of the morphogen. This permits selection of the tissue cell type to be used in the screening. As used herein, "tissue" refers to a group of cells which are naturally found associated, including an organ.

As an example of tissue(s) or organ(s) which produce high levels of morphogen relative to the level produced by other types of tissues, it has been discovered that OP-1, first found in bone tissue is produced at relatively high levels in cells derived

from renal, e.g., kidney or bladder, or adrenal tissue; that GDF-1 is produced at relatively high levels in cells derived from nerve, e.g., brain tissue; that DPP is produced at relatively high levels in cells derived from one of the following drosophila tissues: dorsal ectoderm, epithelial imaginal disc, visceral mesoderm, or gut endoderm; that Vgr-1 is produced at relatively high levels in cells derived from mouse lung tissue; and that Vgl is produced at relatively high levels in cells derived from xenopus fetal endoderm tissue. In addition, BMP3 and CBMP2B transcripts have been identified in abundance in lung tissue. As used herein, "derived" means the cells are the cultured tissue itself, or are a cell line whose parent cells are the tissue itself.

Preferred methods for determining the level of or a change in the level of a morphogen in a cultured cell include using an antibody specific for the morphogen, e.g., in an immunoassay such as an ELISA or radioimmunoassay; and determining the level of nucleic acid, most particularly mRNA, encoding the morphogen using a nucleic acid probe that hybridizes under stringent conditions with the morphogen RNA, such as in an RNA dot blot analysis. Where a change in the presence and/or concentration of morphogen is being determined, it will be necessary to measure and compare the levels of morphogen in the presence and absence of the candidate compound. The nucleic acid probe may be a nucleotide sequence encoding the morphogen or a fragment large enough to hybridize specifically only to RNA encoding a specific morphogen under stringent conditions. As used herein, "stringent conditions" are

defined as conditions in which non-specific hybrids will be eluted but at which specific hybrids will be maintained, i.e., incubation at 0.1X SSC (15mM NaCl, 5mM Na citrate) at 50°C for 15 minutes.

Examples of morphogens whose levels may be determined according to the invention include OP-1, OP-2, GDF-1, Vgr-1, DPP, 60A CBMP2A, CBMP2B, BMP 2, 3, 4, 5, 6, or Vgl. Thus, if an immunoassay is used to indicate the presence and/or concentration of a morphogen, an antibody specific for one of these morphogens only, and which will not detect the presence of other morphogens, will be used. Similarly, if nucleic acid hybridization is used to indicate the level of RNA encoding the morphogen, a nucleotide probe specific for one of these morphogens only will be used under hybridization conditions such that the probe should not be capable of hybridizing with RNA encoding a different morphogen. A morphogen includes an active C-terminal core region, which includes at least six cysteine residues, and a region N-terminal to the C-terminal region that is relatively non-homologous to the equivalent N-terminal regions of other morphogens. In addition, the 3' noncoding region of the mRNA is unique to each morphogen. Thus, a nucleic acid probe encoding all or a portion of the sequences N-terminal to the C-terminal core region of a morphogen, or encoding all or a portion of the sequences C-terminal to or 3' to the core region of a morphogen may be used as a probe which detects mRNA encoding that morphogen only.

"Morphogenic proteins" or "morphogens", as used herein, include naturally-occurring osteogenic proteins

capable of inducing the full developmental cascade of bone formation, as well as polypeptide chains not normally associated with bone or bone formation, but sharing substantial sequence homology with osteogenic proteins. Such proteins, as well as DNA sequences encoding them, have been isolated and characterized for a number of different species. See, for example, U.S. Patent No. 4,968,590 and U.S. Patent Number. 5,011,691, U.S. application Serial Number 1989; 422,699, filed October 17, 1989, and 600,024 and 599,543, both filed October 18, 1990; Sampath et al., (1990) J. Biol. Chem. 265:13198-13205; Ozkaynak et al. (1990) EMBO J. 9:2085-2093; and Lee, Proc. Nat. Aca. Sci. 88:4250-4254 (1991), all of which are hereby incorporated by reference. Many of these proteins subsequently were discovered to have utility beyond bone morphogenesis. See, e.g., USSN 667,274 filed March 11, 1991. The mature forms of morphogens share substantial amino acid sequence homology, especially in the C-terminal core regions of the proteins. In particular, most of the proteins share a seven-cysteine skeleton in this region, in addition to other apparently required amino acids. Table II, infra, shows the amino acid sequence homologies for nine morphogens over the carboxy terminal 102 amino acids.

Among the morphogens useful in this invention are proteins originally identified as osteogenic proteins, such as the OP-1, OP-2 and CBMP2 proteins, as well as amino acid sequence-related proteins such as DPP (from *Drosophila*), Vgl (from *Xenopus*), Vgr-1 (from mouse, see U.S. 5,011,691 to Oppermann et al.), GDF-1 (from mouse, see Lee (1991) PNAS 88:4250-4254), all of which are

presented in Table II and Seq. ID Nos.5-14), and the recently identified 60A protein (from *Drosophila*, Seq. ID No. 24, see Wharton et al. (1991) PNAS 88:9214-9218.) The members of this family, which include members of the TGF- β super-family of proteins, share substantial amino acid sequence homology in their C-terminal regions. The proteins are translated as a precursor, having an N-terminal signal peptide sequence, typically less than about 30 residues, followed by a "pro" domain that is cleaved to yield the mature sequence. The signal peptide is cleaved rapidly upon translation, at a cleavage site that can be predicted in a given sequence using the method of Von Heijne ((1986) Nucleic Acids Research 14:4683-4691.) Table I, below, describes the various morphogens identified to date, including their nomenclature as used herein, their Seq. ID references, and publication sources for the amino acid sequences for the full length proteins not included in the Seq. Listing. The disclosure of these publications is incorporated herein by reference.

TABLE I

"OP-1" refers generically to the group of morphogenically active proteins expressed from part or all of a DNA sequence encoding OP-1 protein, including allelic and species variants thereof, e.g., human OP-1 ("hOP-1", Seq. ID No. 5, mature protein amino acid sequence), or mouse OP-1 ("mOP-1", Seq. ID No. 6, mature protein amino acid sequence.) The

conserved seven cysteine skeleton is defined by residues 38 to 139 of Seq. ID Nos. 5 and 6. The cDNA sequences and the amino acids encoding the full length proteins are provided in Seq. ID Nos. 16 and 17 (hOP1) and Seq. ID Nos. 18 and 19 (mOP1.) The mature proteins are defined by residues 293-431 (hOP1) and 292-430 (mOP1). The "pro" regions of the proteins, cleaved to yield the mature, morphogenically active proteins are defined essentially by residues 30-292 (hOP1) and residues 30-291 (mOP1).

"OP-2"

refers generically to the group of active proteins expressed from part or all of a DNA sequence encoding OP-2 protein, including allelic and species variants thereof, e.g., human OP-2 ("hOP-2", Seq. ID No. 7, mature protein amino acid sequence) or mouse OP-2 ("mOP-2", Seq. ID No. 8, mature protein amino acid sequence). The conserved seven cysteine skeleton is defined by residues 38 to 139 of Seq. ID Nos. 7 and 8. The cDNA sequences and the amino acids encoding the full length proteins are provided in Seq. ID Nos. 20 and 21 (hOP2) and Seq. ID Nos. 22 and 23 (mOP2.) The mature proteins are defined essentially by residues 264-402 (hOP2) and 261-399 (mOP2). The "pro" regions of the proteins, cleaved to yield

the mature, morphogenically active proteins likely are defined essentially by residues 18-263 (hOP2) and residues 18-260 (mOP2). (Another cleavage site also occurs 21 residues upstream for both OP-2 proteins.)

"CBMP2"

refers generically to the morphogenically active proteins expressed from a part or all of a DNA sequence encoding the CBMP2 proteins, including allelic and species variants thereof, e.g., human CBMP2A ("CBMP2A(fx)", Seq ID.No. 9) or human CBMP2B DNA ("CBMP2B(fx)", Seq. ID No. 10). The amino acid sequence for the full length proteins, referred to in the literature as BMP2A and BMP2B, or BMP2 and BMP4, appear in Wozney, et al. (1988) Science 242:1528-1534. The pro domain for BMP2 (BMP2A) likely includes residues 25-248 or 25-282; the mature protein, residues 249-396 or 283-396. The pro domain for BMP4 (BMP2B) likely includes residues 25-256 or 25-292; the mature protein, residues 257-408 or 293-408.

"DPP(fx)"

refers to protein sequences encoded by the *Drosophila* DPP gene and defining the conserved seven cysteine skeleton (Seq. ID No. 11). The amino acid sequence for the full length protein appears in Padgett, et al (1987) Nature 325: 81-84. The pro

domain likely extends from the signal peptide cleavage site to residue 456; the mature protein likely is defined by residues 457-588.

"Vgl(fx)" refers to protein sequences encoded by the *Xenopus Vgl* gene and defining the conserved seven cysteine skeleton (Seq. ID No. 12). The amino acid sequence for the full length protein appears in Weeks (1987) Cell 51: 861-867. The pro domain likely extends from the signal peptide cleavage site to residue 246; the mature protein likely is defined by residues 247-360.

"Vgr-1(fx)" refers to protein sequences encoded by the murine *Vgr-1* gene and defining the conserved seven cysteine skeleton (Seq. ID No. 13). The amino acid sequence for the full length protein appears in Lyons, et al, (1989) PNAS 86: 4554-4558. The pro domain likely extends from the signal peptide cleavage site to residue 299; the mature protein likely is defined by residues 300-438.

"GDF-1(fx)" refers to protein sequences encoded by the human *GDF-1* gene and defining the conserved seven cysteine skeleton (Seq. ID No. 14). The cDNA and encoded amino sequence for the full length protein is

provided in Seq. ID. No. 32. The pro domain likely extends from the signal peptide cleavage site to residue 214; the mature protein likely is defined by residues 215-372.

"60A" refers generically to the morphogenically active proteins expressed from part or all of a DNA sequence (from the *Drosophila* 60A gene) encoding the 60A proteins (see Seq. ID No. 24 wherein the cDNA and encoded amino acid sequence for the full length protein is provided). "60A(fx)" refers to the protein sequences defining the conserved seven cysteine skeleton (residues 354 to 455 of Seq. ID No. 24.) The pro domain likely extends from the signal peptide cleavage site to residue 324; the mature protein likely is defined by residues 325-455.

"BMP3(fx)" refers to protein sequences encoded by the human BMP3 gene and defining the conserved seven cysteine skeleton (Seq. ID No. 26). The amino acid sequence for the full length protein appears in Wozney et al. (1988) Science 242: 1528-1534. The pro domain likely extends from the signal peptide cleavage site to residue 290; the mature protein likely is defined by residues 291-472.

"BMP5(fx)" refers to protein sequences encoded by the human BMP5 gene and defining the conserved seven cysteine skeleton (Seq. ID No. 27). The amino acid sequence for the full length protein appears in Celeste, et al. (1991) PNAS 87: 9843-9847. The pro domain likely extends from the signal peptide cleavage site to residue 316; the mature protein likely is defined by residues 317-454.

"BMP6(fx)" refers to protein sequences encoded by the human BMP6 gene and defining the conserved seven cysteine skeleton (Seq. ID No. 28). The amino acid sequence for the full length protein appear sin Celeste, et al. (1990) PNAS 87: 9843-5847. The pro domain likely includes extends from the signal peptide cleavage site to residue 374; the mature sequence likely includes residues 375-513.

The OP-2 proteins have an additional cysteine residue in this region (e.g., see residue 41 of Seq. ID Nos. 7 and 8), in addition to the conserved cysteine skeleton in common with the other proteins in this family. The GDF-1 protein has a four amino acid insert within the conserved skeleton (residues 44-47 of Seq. ID No. 14) but this insert likely does not interfere with the relationship of the cysteines in the folded

structure. In addition, the CBMP2 proteins are missing one amino acid residue within the cysteine skeleton.

The morphogens are inactive when reduced, but are active as oxidized homodimers and when oxidized in combination with other morphogens of this invention. Thus, as defined herein, a morphogen is a dimeric protein comprising a pair of polypeptide chains, wherein each polypeptide chain comprises at least the C-terminal six cysteine skeleton defined by residues 43-139 of Seq. ID No. 5, including functionally equivalent arrangements of these cysteines (e.g., amino acid insertions or deletions which alter the linear arrangement of the cysteines in the sequence but not their relationship in the folded structure), such that, when the polypeptide chains are folded, the dimeric protein species comprising the pair of polypeptide chains has the appropriate three-dimensional structure, including the appropriate intra- and inter-chain disulfide bonds such that the protein is capable of acting as a morphogen as defined herein. Specifically, the morphogens generally are capable of the following biological functions in a morphogenically permissive environment: stimulating proliferation of progenitor cells; stimulating the differentiation of progenitor cells; stimulating the proliferation of differentiated cells; and supporting the growth and maintenance of differentiated cells, including the "redifferentiation" of transformed cells. In addition, it is also anticipated that these morphogens are capable of

inducing redifferentiation of committed cells under appropriate environmental conditions.

Morphogens useful in this invention comprise one of two species of generic amino acid sequences: Generic Sequence 1 (Seq. ID No. 1) or Generic Sequence 2 (Seq. ID No. 2); where each Xaa indicates one of the 20 naturally-occurring L-isomer, α -amino acids or a derivative thereof. Generic Sequence 1 comprises the conserved six cysteine skeleton and Generic Sequence 2 comprises the conserved six cysteine skeleton plus the additional cysteine identified in OP-2 (see residue 36, Seq. ID No. 2). In another preferred aspect, these sequences further comprise the following additional sequence at their N-terminus:

Cys Xaa Xaa Xaa Xaa (Seq. ID No. 15)
1 5

Preferred amino acid sequences within the foregoing generic sequences include: Generic Sequence 3 (Seq. ID No. 3), Generic Sequence 4 (Seq. ID No. 4), Generic Sequence 5 (Seq. ID No. 30) and Generic Sequence 6 (Seq. ID No. 31), listed below. These Generic Sequences accommodate the homologies shared among the various preferred members of this morphogen family identified in Table II, as well as the amino acid sequence variation among them. Specifically, Generic Sequences 3 and 4 are composite amino acid sequences of the following proteins presented in Table II and identified in Seq. ID Nos. 5-14: human OP-1 (hOP-1, Seq. ID Nos. 5 and 16-17), mouse OP-1 (mOP-1, Seq. ID

Nos. 6 and 18-19), human and mouse OP-2 (Seq. ID Nos. 7, 8, and 20-22), CBMP2A (Seq. ID No. 9), CBMP2B (Seq. ID No. 10), DPP (from Drosophila, Seq. ID No. 11), Vgl, (from Xenopus, Seq. ID No. 12), Vgr-1 (from mouse, Seq. ID No. 13), and GDF-1 (from mouse, Seq. ID No. 14.) The generic sequences include both the amino acid identity shared by the sequences in Table II, as well as alternative residues for the variable positions within the sequence. Note that these generic sequences allow for an additional cysteine at position 41 or 46 in Generic Sequences 3 or 4, respectively, providing an appropriate cysteine skeleton where inter- or intramolecular disulfide bonds can form, and contain certain critical amino acids which influence the tertiary structure of the proteins.

Generic Sequence 3

Leu Tyr Val Xaa Phe

1

5

Xaa Xaa Xaa Gly Trp Xaa Xaa Trp Xaa

10

Xaa Ala Pro Xaa Gly Xaa Xaa Ala

15

20

Xaa Tyr Cys Xaa Gly Xaa Cys Xaa

25

30

Xaa Pro Xaa Xaa Xaa Xaa Xaa

35

Xaa Xaa Xaa Asn His Ala Xaa Xaa

40

45

Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa

50

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys

55

60

Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa

65

Xaa Xaa Xaa Leu Xaa Xaa Xaa

70

75

Xaa Xaa Xaa Xaa Val Xaa Leu Xaa

80

Xaa Xaa Xaa Xaa Met Xaa Val Xaa

85

90

Xaa Cys Gly Cys Xaa

95

wherein each Xaa is independently selected from a group of one or more specified amino acids defined as follows: "Res." means "residue" and Xaa at res.4 = (Ser, Asp or Glu); Xaa at res.6 = (Arg, Gln, Ser or Lys); Xaa at res.7 = (Asp or Glu); Xaa at res.8 = (Leu or Val); Xaa at res.11 = (Gln, Leu, Asp, His or Asn); Xaa at res.12 = (Asp, Arg or Asn); Xaa at res.14 = (Ile or Val); Xaa at res.15 = (Ile or Val); Xaa at res.18 = (Glu, Gln, Leu, Lys, Pro or Arg); Xaa at res.20 = (Tyr or Phe); Xaa at res.21 = (Ala, Ser, Asp, Met, His, Leu or Gln); Xaa at res.23 = (Tyr, Asn or Phe); Xaa at

res.26 = (Glu, His, Tyr, Asp or Gln); Xaa at res.28 = (Glu, Lys, Asp or Gln); Xaa at res.30 = (Ala, Ser, Pro or Gln); Xaa at res.31 = (Phe, Leu or Tyr); Xaa at res.33 = (Leu or Val); Xaa at res.34 = (Asn, Asp, Ala or Thr); Xaa at res.35 = (Ser, Asp, Glu, Leu or Ala); Xaa at res.36 = (Tyr, Cys, His, Ser or Ile); Xaa at res.37 = (Met, Phe, Gly or Leu); Xaa at res.38 = (Asn or Ser); Xaa at res.39 = (Ala, Ser or Gly); Xaa at res.40 = (Thr, Leu or Ser); Xaa at res.44 = (Ile or Val); Xaa at res.45 = (Val or Leu); Xaa at res.46 = (Gln or Arg); Xaa at res.47 = (Thr, Ala or Ser); Xaa at res.49 = (Val or Met); Xaa at res.50 = (His or Asn); Xaa at res.51 = (Phe, Leu, Asn, Ser, Ala or Val); Xaa at res.52 = (Ile, Met, Asn, Ala or Val); Xaa at res.53 = (Asn, Lys, Ala or Glu); Xaa at res.54 = (Pro or Ser); Xaa at res.55 = (Glu, Asp, Asn, or Gly); Xaa at res.56 = (Thr, Ala, Val, Lys, Asp, Tyr, Ser or Ala); Xaa at res.57 = (Val, Ala or Ile); Xaa at res.58 = (Pro or Asp); Xaa at res.59 = (Lys or Leu); Xaa at res.60 = (Pro or Ala); Xaa at res.63 = (Ala or Val); Xaa at res.65 = (Thr or Ala); Xaa at res.66 = (Gln, Lys, Arg or Glu); Xaa at res.67 = (Leu, Met or Val); Xaa at res.68 = (Asn, Ser or Asp); Xaa at res.69 = (Ala, Pro or Ser); Xaa at res.70 = (Ile, Thr or Val); Xaa at res.71 = (Ser or Ala); Xaa at res.72 = (Val or Met); Xaa at res.74 = (Tyr or Phe); Xaa at res.75 = (Phe, Tyr or Leu); Xaa at res.76 = (Asp or Asn); Xaa at res.77 = (Asp, Glu, Asn or Ser); Xaa at res.78 = (Ser, Gln, Asn or Tyr); Xaa at res.79 = (Ser, Asn, Asp or Glu); Xaa at res.80 = (Asn, Thr or Lys); Xaa at res.82 = (Ile or Val); Xaa at res.84 = (Lys or Arg); Xaa at res.85 = (Lys, Asn, Gln or His); Xaa at res.86 = (Tyr or His);

Xaa at res.87 = (Arg, Gln or Glu); Xaa at res.88 = (Asn, Glu or Asp); Xaa at res.90 = (Val, Thr or Ala); Xaa at res.92 = (Arg, Lys, Val, Asp or Glu); Xaa at res.93 = (Ala, Gly or Glu); and Xaa at res.97 = (His or Arg);

Generic Sequence 4

Cys	Xaa	Xaa	Xaa	Xaa	Leu	Tyr	Val	Xaa	Phe		
1					5				10		
Xaa	Xaa	Xaa	Gly	Trp	Xaa	Xaa	Trp	Xaa			
					15						
Xaa	Ala	Pro	Xaa	Gly	Xaa	Xaa	Ala				
20					25						
Xaa	Tyr	Cys	Xaa	Gly	Xaa	Cys	Xaa				
		30					35				
Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa				
					40						
Xaa	Xaa	Xaa	Asn	His	Ala	Xaa	Xaa				
			45				50				
Xaa	Xaa	Leu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa			
					55						
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys			
		60					65				
Cys	Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa			
					70						
Xaa	Xaa	Xaa	Leu	Xaa	Xaa	Xaa					
75					80						
Xaa	Xaa	Xaa	Xaa	Val	Xaa	Leu	Xaa				
					85						
Xaa	Xaa	Xaa	Xaa	Met	Xaa	Val	Xaa				
90					95						

Xaa Cys Gly Cys Xaa

100

wherein each Xaa is independently selected from a group of one or more specified amino acids as defined by the following: "Res." means "residue" and Xaa at res.2 = (Lys or Arg); Xaa at res.3 = (Lys or Arg); Xaa at res.4 = (His or Arg); Xaa at res.5 = (Glu, Ser, His, Gly, Arg or Pro); Xaa at res.9 = (Ser, Asp or Glu); Xaa at res.11 = (Arg, Gln, Ser or Lys); Xaa at res.12 = (Asp or Glu); Xaa at res.13 = (Leu or Val); Xaa at res.16 = (Gln, Leu, Asp, His or Asn); Xaa at res.17 = (Asp, Arg, or Asn); Xaa at res.19 = (Ile or Val); Xaa at res.20 = (Ile or Val); Xaa at res.23 = (Glu, Gln, Leu, Lys, Pro or Arg); Xaa at res.25 = (Tyr or Phe); Xaa at res.26 = (Ala, Ser, Asp, Met, His, Leu, or Gln); Xaa at res.28 = (Tyr, Asn or Phe); Xaa at res.31 = (Glu, His, Tyr, Asp or Gln); Xaa at res.33 = Glu, Lys, Asp or Gln; Xaa at res.35 = (Ala, Ser or Pro); Xaa at res.36 = (Phe, Leu or Tyr); Xaa at res.38 = (Leu or Val); Xaa at res.39 = (Asn, Asp, Ala or Thr); Xaa at res.40 = (Ser, Asp, Glu, Leu or Ala); Xaa at res.41 = (Tyr, Cys, His, Ser or Ile); Xaa at res.42 = (Met, Phe, Gly or Leu); Xaa at res.44 = (Ala, Ser or Gly); Xaa at res.45 = (Thr, Leu or Ser); Xaa at res.49 = (Ile or Val); Xaa at res.50 = (Val or Leu); Xaa at res.51 = (Gln or Arg); Xaa at res.52 = (Thr, Ala or Ser); Xaa at res.54 = (Val or Met); Xaa at res.55 = (His or Asn); Xaa at res.56 = (Phe, Leu, Asn, Ser, Ala or Val); Xaa at res.57 = (Ile, Met, Asn, Ala or Val); Xaa at res.58 = (Asn, Lys, Ala or Glu); Xaa at res.59 = (Pro or Ser); Xaa at res.60 = (Glu, Asp, or Gly); Xaa at res.61 = (Thr, Ala, Val, Lys, Asp, Tyr, Ser or Ala); Xaa at res.62 = (Val, Ala

or Ile); Xaa at res.63 = (Pro or Asp); Xaa at res.64 = (Lys or Leu); Xaa at res.65 = (Pro or Ala); Xaa at res.68 = (Ala or Val); Xaa at res.70 = (Thr or Ala); Xaa at res.71 = (Gln, Lys, Arg or Glu); Xaa at res.72 = (Leu, Met or Val); Xaa at res.73 = (Asn, Ser or Asp); Xaa at res.74 = (Ala, Pro or Ser); Xaa at res.75 = (Ile, Thr or Val); Xaa at res.76 = (Ser or Ala); Xaa at res.77 = (Val or Met); Xaa at res.79 = (Tyr or Phe); Xaa at res.80 = (Phe, Tyr or Leu); Xaa at res.81 = (Asp or Asn); Xaa at res.82 = (Asp, Glu, Asn or Ser); Xaa at res.83 = (Ser, Gln, Asn or Tyr); Xaa at res.84 = (Ser, Asn, Asp or Glu); Xaa at res.85 = (Asn, Thr or Lys); Xaa at res.87 = (Ile or Val); Xaa at res.89 = (Lys or Arg); Xaa at res.90 = (Lys, Asn, Gln or His); Xaa at res.91 = (Tyr or His); Xaa at res.92 = (Arg, Gln or Glu); Xaa at res.93 = (Asn, Glu or Asp); Xaa at res.95 = (Val, Thr or Ala); Xaa at res.97 = (Arg, Lys, Val, Asp or Glu); Xaa at res.98 = (Ala, Gly or Glu); and Xaa at res.102 = (His or Arg).

Similarly, Generic Sequence 5 (Seq. ID No. 30) and Generic Sequence 6 (Seq. ID No. 31) accommodate the homologies shared among all the morphogen protein family members identified in Table II. Specifically, Generic Sequences 5 and 6 are composite amino acid sequences of human OP-1 (hOP-1, Seq. ID Nos. 5 and 16-17), mouse OP-1 (mOP-1, Seq. ID Nos. 6 and 18-19), human and mouse OP-2 (Seq. ID Nos. 7, 8, and 20-22), CBMP2A (Seq. ID No. 9), CBMP2B (Seq. ID No. 10), DPP (from *Drosophila*, Seq. ID No. 11), Vgl, (from *Xenopus*, Seq. ID No. 12), Vgr-1 (from mouse, Seq. ID No. 13), and GDF-1 (from mouse, Seq. ID No. 14), human BMP3

(Seq. ID No. 26), human BMP5 (Seq. ID No. 27), human BMP6 (Seq. ID No. 28) and 60(A) (from *Drosophila*, Seq. ID Nos. 24-25). The generic sequences include both the amino acid identity shared by these sequences in the C-terminal domain, defined by the six and seven cysteine skeletons (Generic Sequences 5 and 6, respectively), as well as alternative residues for the variable positions within the sequence. As for Generic Sequences 3 and 4, Generic Sequences 5 and 6 allow for an additional cysteine at position 41 (Generic Sequence 5) or position 46 (Generic Sequence 6), providing an appropriate cysteine skeleton where inter- or intramolecular disulfide bonds can form, and containing certain critical amino acids which influence the tertiary structure of the proteins.

Generic Sequence 5

```

      Leu Xaa Xaa Xaa Phe
      1               5
Xaa Xaa Xaa Gly Trp Xaa Xaa Trp Xaa
      10
Xaa Xaa Pro Xaa Xaa Xaa Xaa Ala
      15               20
Xaa Tyr Cys Xaa Gly Xaa Cys Xaa
      25               30
Xaa Pro Xaa Xaa Xaa Xaa Xaa
      35

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Xaa Xaa Xaa Asn His Ala Xaa Xaa

40

45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

50

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys

55

60

Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa

65

Xaa Xaa Xaa Leu Xaa Xaa Xaa

70

75

Xaa Xaa Xaa Xaa Val Xaa Leu Xaa

80

Xaa Xaa Xaa Xaa Met Xaa Val Xaa

85

90

Xaa Cys Xaa Cys Xaa

95

wherein each Xaa is independently selected from a group of one or more specified amino acids defined as follows: "Res." means "residue" and Xaa at res.2 = (Tyr or Lys); Xaa at res.3 = Val or Ile); Xaa at res.4 = (Ser, Asp or Glu); Xaa at res.6 = (Arg, Gln, Ser, Lys or Ala); Xaa at res.7 = (Asp, Glu or Lys); Xaa at res.8 = (Leu, Val or Ile); Xaa at res.11 = (Gln, Leu, Asp, His, Asn or Ser); Xaa at res.12 = (Asp, Arg, Asn or Glu); Xaa at res.14 = (Ile or Val); Xaa at res.15 = (Ile or Val); Xaa at res.16 (Ala or Ser); Xaa at res.18 = (Glu, Gln, Leu, Lys, Pro or Arg); Xaa at res.19 =

(Gly or Ser); Xaa at res.20 = (Tyr or Phe); Xaa at res.21 = (Ala, Ser, Asp, Met, His, Gln, Leu or Gly); Xaa at res.23 = (Tyr, Asn or Phe); Xaa at res.26 = (Glu, His, Tyr, Asp, Gln or Ser); Xaa at res.28 = (Glu, Lys, Asp, Gln or Ala); Xaa at res.30 = (Ala, Ser, Pro, Gln or Asn); Xaa at res.31 = (Phe, Leu or Tyr); Xaa at res.33 = (Leu, Val or Met); Xaa at res.34 = (Asn, Asp, Ala, Thr or Pro); Xaa at res.35 = (Ser, Asp, Glu, Leu, Ala or Lys); Xaa at res.36 = (Tyr, Cys, His, Ser or Ile); Xaa at res.37 = (Met, Phe, Gly or Leu); Xaa at res.38 = (Asn, Ser or Lys); Xaa at res.39 = (Ala, Ser, Gly or Pro); Xaa at res.40 = (Thr, Leu or Ser); Xaa at res.44 = (Ile, Val or Thr); Xaa at res.45 = (Val, Leu or Ile); Xaa at res.46 = (Gln or Arg); Xaa at res.47 = (Thr, Ala or Ser); Xaa at res.48 = (Leu or Ile); Xaa at res.49 = (Val or Met); Xaa at res.50 = (His, Asn or Arg); Xaa at res.51 = (Phe, Leu, Asn, Ser, Ala or Val); Xaa at res.52 = (Ile, Met, Asn, Ala, Val or Leu); Xaa at res.53 = (Asn, Lys, Ala, Glu, Gly or Phe); Xaa at res.54 = (Pro, Ser or Val); Xaa at res.55 = (Glu, Asp, Asn, Gly, Val or Lys); Xaa at res.56 = (Thr, Ala, Val, Lys, Asp, Tyr, Ser, Ala, Pro or His); Xaa at res.57 = (Val, Ala or Ile); Xaa at res.58 = (Pro or Asp); Xaa at res.59 = (Lys, Leu or Glu); Xaa at res.60 = (Pro or Ala); Xaa at res.63 = (Ala or Val); Xaa at res.65 = (Thr, Ala or Glu); Xaa at res.66 = (Gln, Lys, Arg or Glu); Xaa at res.67 = (Leu, Met or Val); Xaa at res.68 = (Asn, Ser, Asp or Gly); Xaa at res.69 = (Ala, Pro or Ser); Xaa at res.70 = (Ile, Thr, Val or Leu); Xaa at res.71 = (Ser, Ala or Pro); Xaa at res.72 = (Val, Met or Ile); Xaa at res.74 = (Tyr or Phe); Xaa at res.75 = (Phe, Tyr, Leu or His); Xaa at res.76 = (Asp, Asn or

Leu); Xaa at res.77 = (Asp, Glu, Asn or Ser); Xaa at res.78 = (Ser, Gln, Asn, Tyr or Asp); Xaa at res.79 = (Ser, Asn, Asp, Glu or Lys); Xaa at res.80 = (Asn, Thr or Lys); Xaa at res.82 = (Ile, Val or Asn); Xaa at res.84 = (Lys or Arg); Xaa at res.85 = (Lys, Asn, Gln, His or Val); Xaa at res.86 = (Tyr or His); Xaa at res.87 = (Arg, Gln, Glu or Pro); Xaa at res.88 = (Asn, Glu or Asp); Xaa at res.90 = (Val, Thr, Ala or Ile); Xaa at res.92 = (Arg, Lys, Val, Asp or Glu); Xaa at res.93 = (Ala, Gly, Glu or Ser); Xaa at res.95 = (Gly or Ala) and Xaa at res.97 = (His or Arg).

Generic Sequence 6

Cys	Xaa	Xaa	Xaa	Xaa	Leu	Xaa	Xaa	Xaa	Phe
1				5					10
Xaa	Xaa	Xaa	Gly	Trp	Xaa	Xaa	Trp	Xaa	
				15					
Xaa	Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Ala		
20					25				
Xaa	Tyr	Cys	Xaa	Gly	Xaa	Cys	Xaa		
		30					35		
Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Xaa			
				40					
Xaa	Xaa	Xaa	Asn	His	Ala	Xaa	Xaa		
		45					50		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
				55					
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys		
60							65		
Cys	Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Xaa		
				70					

```

Xaa Xaa Xaa Leu Xaa Xaa Xaa
 75                               80
Xaa Xaa Xaa Xaa Val Xaa Leu Xaa
                        85
Xaa Xaa Xaa Xaa Met Xaa Val Xaa
 90                               95
Xaa Cys Xaa Cys Xaa
                        100

```

wherein each Xaa is independently selected from a group of one or more specified amino acids as defined by the following: "Res." means "residue" and Xaa at res.2 = (Lys, Arg, Ala or Gln); Xaa at res.3 = (Lys, Arg or Met); Xaa at res.4 = (His, Arg or Gln); Xaa at res.5 = (Glu, Ser, His, Gly, Arg, Pro, Thr, or Tyr); Xaa at res.7 = (Tyr or Lys); Xaa at res.8 = (Val or Ile); Xaa at res.9 = (Ser, Asp or Glu); Xaa at res.11 = (Arg, Gln, Ser, Lys or Ala); Xaa at res.12 = (Asp, Glu, or Lys); Xaa at res.13 = (Leu, Val or Ile); Xaa at res.16 = (Gln, Leu, Asp, His, Asn or Ser); Xaa at res.17 = (Asp, Arg, Asn or Glu); Xaa at res.19 = (Ile or Val); Xaa at res.20 = (Ile or Val); Xaa at res.21 = (Ala or Ser); Xaa at res.23 = (Glu, Gln, Leu, Lys, Pro or Arg); Xaa at res.24 = (Gly or Ser); Xaa at res.25 = (Tyr or Phe); Xaa at res.26 = (Ala, Ser, Asp, Met, His, Gln, Leu, or Gly); Xaa at res.28 = (Tyr, Asn or Phe); Xaa at res.31 = (Glu, His, Tyr, Asp, Gln or Ser); Xaa at res.33 = Glu, Lys, Asp, Gln or Ala); Xaa at res.35 = (Ala, Ser, Pro, Gln or Asn); Xaa at res.36 = (Phe, Leu or Tyr); Xaa at res.38 = (Leu, Val or Met); Xaa at res.39 = (Asn, Asp, Ala, Thr or Pro); Xaa at res.40 = (Ser, Asp, Glu, Leu, Ala or Lys); Xaa at res.41 = (Tyr,

Cys, His, Ser or Ile); Xaa at res.42 = (Met, Phe, Gly or Leu); Xaa at res.43 = (Asn, Ser or Lys); Xaa at res.44 = (Ala, Ser, Gly or Pro); Xaa at res.45 = (Thr, Leu or Ser); Xaa at res.49 = (Ile, Val or Thr); Xaa at res.50 = (Val, Leu or Ile); Xaa at res.51 = (Gln or Arg); Xaa at res.52 = (Thr, Ala or Ser); Xaa at res.53 = (Leu or Ile); Xaa at res.54 = (Val or Met); Xaa at res.55 = (His, Asn or Arg); Xaa at res.56 = (Phe, Leu, Asn, Ser, Ala or Val); Xaa at res.57 = (Ile, Met, Asn, Ala, Val or Leu); Xaa at res.58 = (Asn, Lys, Ala, Glu, Gly or Phe); Xaa at res.59 = (Pro, Ser or Val); Xaa at res.60 = (Glu, Asp, Gly, Val or Lys); Xaa at res.61 = (Thr, Ala, Val, Lys, Asp, Tyr, Ser, Ala, Pro or His); Xaa at res.62 = (Val, Ala or Ile); Xaa at res.63 = (Pro or Asp); Xaa at res.64 = (Lys, Leu or Glu); Xaa at res.65 = (Pro or Ala); Xaa at res.68 = (Ala or Val); Xaa at res.70 = (Thr, Ala or Glu); Xaa at res.71 = (Gln, Lys, Arg or Glu); Xaa at res.72 = (Leu, Met or Val); Xaa at res.73 = (Asn, Ser, Asp or Gly); Xaa at res.74 = (Ala, Pro or Ser); Xaa at res.75 = (Ile, Thr, Val or Leu); Xaa at res.76 = (Ser, Ala or Pro); Xaa at res.77 = (Val, Met or Ile); Xaa at res.79 = (Tyr or Phe); Xaa at res.80 = (Phe, Tyr, Leu or His); Xaa at res.81 = (Asp, Asn or Leu); Xaa at res.82 = (Asp, Glu, Asn or Ser); Xaa at res.83 = (Ser, Gln, Asn, Tyr or Asp); Xaa at res.84 = (Ser, Asn, Asp, Glu or Lys); Xaa at res.85 = (Asn, Thr or Lys); Xaa at res.87 = (Ile, Val or Asn); Xaa at res.89 = (Lys or Arg); Xaa at res.90 = (Lys, Asn, Gln, His or Val); Xaa at res.91 = (Tyr or His); Xaa at res.92 = (Arg, Gln, Glu or Pro); Xaa at res.93 = (Asn, Glu or Asp); Xaa at res.95 = (Val, Thr, Ala or Ile); Xaa at res.97 = (Arg, Lys, Val,

Asp or Glu); Xaa at res.98 = (Ala, Gly, Glu or Ser); Xaa at res.100 = (Gly or Ala); and Xaa at res.102 = (His or Arg).

Particularly useful sequences for use as morphogens in this invention include the C-terminal domains, e.g., the C-terminal 96-102 amino acid residues of Vgl, Vgr-1, DPP, OP-1, OP-2, CBMP-2A, CBMP-2B, GDF-1 (see Table II, below, and Seq. ID Nos. 5-14), as well as proteins comprising the C-terminal domains of 60A, BMP3, BMP5 and BMP6 (see Seq. ID Nos. 24-28), all of which include at least the conserved six or seven cysteine skeleton. In addition, biosynthetic constructs designed from the generic sequences, such as COP-1, 3-5, 7, 16, disclosed in U.S. Pat. No. 5,011,691, also are useful. Other sequences include the inhibins/activin proteins (see, for example, U.S. Pat. Nos. 4,968,590 and 5,011,691). Accordingly, other useful sequences are those sharing at least 70% amino acid sequence homology or "similarity", and preferably 80% homology or similarity with any of the sequences above. These are anticipated to include allelic and species variants and mutants, and biosynthetic muteins, as well as novel members of this morphogenic family of proteins. Particularly envisioned in the family of related proteins are those proteins exhibiting morphogenic activity and wherein the amino acid changes from the preferred sequences include conservative changes, e.g., those as defined by Dayoff et al., Atlas of Protein Sequence and Structure; vol. 5, Suppl. 3, pp. 345-362, (M.O. Dayoff, ed., Nat'l BioMed. Research Fdn., Washington, D.C. 1979). As used

herein, potentially useful sequences are aligned with a known morphogen sequence using the method of Needleman et al. ((1970) J.Mol.Biol. 48:443-453) and identities calculated by the Align program (DNASTar, Inc.). "Homology" or "similarity" as used herein includes allowed conservative changes as defined by Dayoff et al.

Morphogen sequences which are detectable according to the methods of the invention include but are not limited to those having greater than 60% identity, preferably greater than 65% identity, with the amino acid sequence defining the conserved six cysteine skeleton of hOP1 (e.g., residues 43-139 of Seq. ID No. 5). These most preferred sequences include both allelic and species variants of the OP-1 and OP-2 proteins, including the Drosophila 60A protein. Accordingly, morphogens which are detectable according to the invention include active proteins comprising species of polypeptide chains having the generic amino acid sequence herein referred to as "OPX", which accommodates the homologies between the various identified species of OP1 and OP2 (Seq. ID No. 29).

The morphogens detectable in the methods of this invention include proteins comprising any of the polypeptide chains described above, whether isolated from naturally-occurring sources, or produced by recombinant DNA or other synthetic techniques, and includes allelic and species variants of these proteins, naturally-occurring or biosynthetic mutants thereof, chimeric variants containing a domain(s) or

region(s) of one family member functionally arranged with another domain(s) or regions(s) of a second family member, as well as various truncated and fusion constructs. Deletion or insertion or addition mutants also are envisioned to be active, including those which may alter the conserved C-terminal cysteine skeleton, provided that the alteration does not functionally disrupt the relationship of these cysteines in the folded structure. Accordingly, such active forms are considered the equivalent of the specifically described constructs disclosed herein. The proteins may include forms having varying glycosylation patterns, varying N-termini, a family of related proteins having regions of amino acid sequence homology, and active truncated or mutated forms of native or biosynthetic proteins, produced by expression of recombinant DNA in host cells.

The morphogenic proteins can be expressed from intact or truncated cDNA or from synthetic DNAs in procaryotic or eucaryotic host cells, and purified, cleaved, refolded, and dimerized to form morphogenically active compositions. Currently preferred host cells include E. coli or mammalian cells, such as CHO, COS or BSC cells. A detailed description of the morphogens detectable according to the methods of this invention is disclosed in copending US patent application Serial Nos. 752,764, filed August 30, 1991, and 667,274, filed March 11, 1991, the disclosure of which are incorporated herein by reference.

The screening method of the invention provides a simple method of determining a change in the level of morphogenic protein as a result of exposure of cultured cells to one or more compound(s). The level of a morphogenic protein in a given cell culture, or a change in that level resulting from exposure to one or more compound(s) indicates that direct application of the compound modulates the level of the morphogen expressed by the cultured cells. If, for example, a compound upregulated the production of OP-1 by a kidney cell line, it would then be desirable to test systemic administration of this compound in an animal model to determine if it upregulated the production of OP-1 in vivo. If this compound did upregulate the endogenous circulating levels of OP-1, it would be consistent with administration of the compound systemically for the purpose of correcting bone metabolism diseases such as osteoporosis. The level of morphogen in the body may be a result of a wide range of physical conditions, e.g., tissue degeneration such as occurs in diseases including arthritis, emphysema, osteoporosis, kidney diseases, lung diseases, cardiomyopathy, and cirrhosis of the liver. The level of morphogens in the body may also occur as a result of the normal process of aging. A compound selected by the screening method of the invention as, for example, one which increases the level of morphogen in a tissue, may be consistent with the administration of the compound systemically or locally to a tissue for the purpose of preventing some form of tissue degeneration or for restoring the degenerated tissue to its normal healthy level.

Other advantages of the invention include determining the tissue or tissues of origin of a given morphogen in order to administer a compound aimed at modulating the systemic level of morphogen for treatment of a disease or condition in which the level of morphogen production has become altered.

Brief Description of the Drawings

Fig. 1 shows the fragments of OP-1, used as probes in Northern hybridizations useful in the processes of the invention.

Fig. 2 shows results of Northern blot analysis of RNA using different OP-1-specific probes.

Fig. 3 shows results of Northern blot analysis of RNA from different cells types probed with an OP-1 probe.

Detailed Description

The invention is based on the discovery of a family of structurally related morphogenic proteins (BMPs), also called osteogenic proteins (OPs), and more particularly that various of these proteins play an important role, not only in embryogenesis, but also in tissue and organ maintenance and repair in juvenile and adult mammals. Morphogenic proteins which have been identified include BMP 2, 3, 4, 5, 6, OP-1 and OP-2 (murine and human), Vgr-1, Vgl, DPP, GDF-1, CMBP-2A, CMBP-2B, 60A, and the inhibin/activin class of proteins. Other recombinant proteins include COP1, COP3, COP4, COP5, COP7, and COP16. While, as explained herein, the morphogen have significant homologies and similarities in structure, it is hypothesized that variants within the morphogenic protein genes may have specific roles in specific tissue involving, for example, stimulation of progenitor cell multiplication, tissue specific or tissue preferred phenotype maintenance, and/or stimulation or modulation of the rate of differentiation, growth or replication of tissue cells characterized by high turnover. The effect on the long-term physiology, maintenance and repair of particular tissues by particular species of the morphogens is currently unknown in any significant detail. However, methods useful in determining which particular tissues express which particular morphogen(s), and for finding changes which stimulate or depress morphogen expression in vivo, would enable discovery and development of strategies for therapeutic treatment of a large number of diseased states, and provide drugs designed to implement the strategy.

This invention provides such methods and, more specifically, two generic processes for obtaining data which ultimately will permit determination of structure/activity relationships of specific naturally occurring mammalian morphogens and drugs capable of modulating their production. For example, using the assay of the invention, it has been determined that OP-1, first found in bone and demonstrated to be osteoinductive, is synthesized primarily in kidney, bladder, and adrenal tissue. This surprising discovery, coupled with the observation that patients with kidney disease often express loss of bone mass, suggests that the bone loss in these patients may be due to pathologic depression of OP-1 synthesis in kidney, and suggests that administration of OP-1 systemically or stimulation of OP-1 expression and secretion by the kidney may arrest bone loss, or effect remineralization through increased bone formation (i.e., osteogenesis).

There are two fundamental aspects of the invention. One aspect involves an assay to determine tissues and cell types capable of synthesis and secretion of the morphogens; the other involves the use of the identified cell types configured in a screening system to find substances useful therapeutically to modulate, i.e., stimulate or depress, morphogen expression and/or secretion.

The assay to determine the tissue of origin of a given morphogen involves screening a plurality (i.e., two or more) different tissues by determining a parameter indicative of production of a morphogen in the tissue, and comparing the parameters. The tissue(s) of origin will, of course, be the tissue that produces that morphogen.

The other assay of the invention involves screening candidate compounds for their ability to modulate the effective systemic or local concentration of a morphogen by incubating the compound with a cell culture that produces the morphogen, and assaying the culture for a parameter indicative of a change in the production level of the morphogen. Useful candidate compounds then may be tested for in vivo efficacy in a suitable animal model. These compounds then may be used in vivo to modulate effective morphogen concentrating in the disease treatment.

1. Morphogen Tissue Distribution

Morphogens are broadly distributed in developing and adult tissue. For example, DPP and 60A are expressed in both embryonic and developing *Drosophila* tissue. Vgl has been identified in *Xenopus* embryonic tissue. Vgr-1 transcripts have been identified in a variety of murine tissues, including embryonic and developing brain, lung, liver, kidney and calvaria (dermal bone) tissue. In addition, both CBMP2B and CBMP3 have been identified in lung tissue. Recently, Vgr-1 transcripts also have been identified in adult murine lung, kidney, heart, and brain tissue, with particularly high levels in the lung (see *infra*). GDF-1 has been identified in human adult cerebellum and in fetal brain tissue. In addition, recent Northern blot analyses indicate that OP-1 is encoded by multiple transcripts in different tissues. This potential alternative splicing is consistent with the hypothesis that the longer transcripts may encoded additional proteins (e.g., bicistronic mRNA) and each form may be tissue or developmentally related.

OP-1 and the CBMP2 proteins, both first identified as bone morphogens, have been identified in mouse and human placenta, hippocampus, calvaria and osteosarcoma tissue as determined by identification of OP-1 and CMBP2-specific sequences in cDNA libraries constructed from these tissues (see USSN 422,699, incorporated herein by reference). Additionally, the OP-1 protein is present in a variety of embryonic and developing tissues including kidney, liver, heart and brain as determined by Western blot analysis and immunolocalization (see *infra*). OP-1-specific transcripts also have been identified in both embryonic and developing tissues, most abundantly in developing kidney, bladder, adrenal and (see *infra*). OP-1 also has been identified as a mesoderm inducing factor present during embryogenesis. Moreover, OP-1 has been shown to be associated with satellite cells in the muscle and associated with potential pluripotential stem cells in bone marrow following damage to adult murine endochondral bone, indicating its morphogenic role in tissue repair and regeneration. In addition, a novel protein GDF-1 comprising a 7 cysteine skeleton, has been identified in neural tissue (Lee, 1991, *Proc. Nat. Aca. Sci.* 88: 4250-4254).

Knowledge of the tissue distribution of a given morphogen may be useful in choosing a cell type for screening according to the invention, or for targeting that cell type or tissue type for treatment. The proteins (or their mRNA transcripts) are readily identified in different tissues using standard methodologies and minor modifications thereof in tissues where expression may be low. For example, protein distribution may be determined using standard Western blot analysis or immunocytochemical techniques, and antibodies specific to the morphogen or

morphogens of interest. Similarly, the distribution of morphogen transcripts may be determined using standard Northern hybridization protocols and a transcript-specific probe and hybridization conditions.

2. Useful Morphogens

As defined herein a protein is morphogenic if it is capable of inducing the developmental cascade of cellular and molecular events that culminate in the formation of new, organ-specific tissue and comprises at least the conserved C-terminal six cysteine skeleton or its functional equivalent (see supra). Specifically, the morphogens generally are capable of all of the following biological functions in a morphogenically permissive environment: stimulating proliferation of progenitor cells; stimulating the differentiation of progenitor cells; stimulating the proliferation of differentiated cells; and supporting the growth and maintenance of differentiated cells, including the "redifferentiation" of transformed cells. Details of how the morphogens detectable according to the methods of this invention first were identified, as well as a description on how to make, use and test them for morphogenic activity are disclosed in USSN 667,274, filed March 11, 1991 and USSN 752,764, filed August 30, 1991, the disclosures of which are hereby incorporated by reference. As disclosed therein, the morphogens may be purified from naturally-sourced material or recombinantly produced from procaryotic or eucaryotic host cells, using the genetic sequences disclosed therein. Alternatively, novel morphogenic sequences may be identified following the procedures disclosed therein.

Particularly useful proteins include those which comprise the naturally derived sequences disclosed in Table II. Other useful sequences include biosynthetic constructs such as those disclosed in U.S. Pat. 5,011,691, the disclosure of which is incorporated herein by reference (e.g., COP-1, COP-3, COP-4, COP-5, COP-7, and COP-16).

Accordingly, the morphogens detectable according to the methods and compositions of this invention also may be described by morphogenically active proteins having amino acid sequences sharing 70% or, preferably, 80% homology (similarity) with any of the sequences described above, where "homology" is as defined herein above.

The morphogens detectable according to the method of this invention also can be described by any of the 6 generic sequences described herein (Generic Sequences 1, 2, 3, 4, 5 and 6). Generic sequences 1 and 2 also may include, at their N-terminus, the sequence

Cys Xaa Xaa Xaa Xaa (Seq. ID No. 15)

1

5

Table II, set forth below, compares the amino acid sequences of the active regions of native proteins that have been identified as morphogens, including human OP-1 (hOP-1, Seq. ID Nos. 5 and 16-17), mouse OP-1 (mOP-1, Seq. ID Nos. 6 and 18-19), human and mouse OP-2 (Seq. ID Nos. 7, 8, and 20-23), CBMP2A (Seq. ID No. 9), CBMP2B (Seq. ID No. 10), BMP3 (Seq. ID No. 26), DPP (from *Drosophila*, Seq. ID No. 11), Vgl, (from *Xenopus*, Seq. ID No. 12), Vgr-1 (from mouse, Seq. ID No. 13), GDF-1 (from mouse, Seq. ID

Nos. 14, 32 and 33), 60A protein (from *Drosophila*, Seq. ID Nos. 24 and 25), BMP5 (Seq. ID No. 27) and BMP6 (Seq. ID No. 28). The sequences are aligned essentially following the method of Needleman et al. (1970) J. Mol. Biol., 48:443-453, calculated using the Align Program (DNASTAR, Inc.) In the table, three dots indicates that the amino acid in that position is the same as the amino acid in hOP-1. Three dashes indicates that no amino acid is present in that position, and are included for purposes of illustrating homologies. For example, amino acid residue 60 of CBMP-2A and CBMP-2B is "missing". Of course, both these amino acid sequences in this region comprise Asn-Ser (residues 58, 59), with CBMP-2A then comprising Lys and Ile, whereas CBMP-2B comprises Ser and Ile.

TABLE II

hOP-1	Cys	Lys	Lys	His	Glu	Leu	Tyr	Val
mOP-1
hOP-2	...	Arg	Arg
mOP-2	...	Arg	Arg
DPP	...	Arg	Arg	...	Ser
Vgl	Lys	Arg	His
Vgr-1	Gly
CBMP-2A	Arg	...	Pro
CBMP-2B	...	Arg	Arg	...	Ser
BMP3	...	Ala	Arg	Arg	Tyr	...	Lys	...
GDF-1	...	Arg	Ala	Arg	Arg
60A	...	Gln	Met	Glu	Thr
BMP5
BMP6	...	Arg
	1				5			

hOP-1	Ser	Phe	Arg	Asp	Leu	Gly	Trp	Gln	Asp
mOP-1
hOP-2	Gln	Leu	...
mOP-2	Ser	Leu	...
DPP	Asp	...	Ser	...	Val	Asp	...
Vgl	Glu	...	Lys	...	Val	Asn
Vgr-1	Gln	...	Val
CBMP-2A	Asp	...	Ser	...	Val	Asn	...
CBMP-2B	Asp	...	Ser	...	Val	Asn	...
BMP3	Asp	...	Ala	...	Ile	Ser	Glu
GDF-1	Glu	Val	His	Arg
60A	Asp	...	Lys	His	...

BMP5
BMP6	Gln
		10					15		

hOP-1	Trp	Ile	Ile	Ala	Pro	Glu	Gly	Tyr	Ala
mOP-1
hOP-2	...	Val	Gln	Ser
mOP-2	...	Val	Gln	Ser
DPP	Val	Leu	Asp
Vgl	...	Val	Gln	Met
Vgr-1	Lys
CBMP-2A	Val	Pro	His
CBMP-2B	Val	Pro	Gln
BMP3	Ser	...	Lys	Ser	Phe	Asp
GDF-1	...	Val	Arg	...	Phe	Leu
60A	Gly
BMP5
BMP6	Lys
			20					25	

hOP-1	Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ala
mOP-1
hOP-2	Ser
mOP-2
DPP	His	...	Lys	...	Pro
Vgl	...	Asn	Tyr	Pro
Vgr-1	...	Asn	Asp	Ser
CBMP-2A	...	Phe	His	...	Glu	...	Pro
CBMP-2B	...	Phe	His	...	Asp	...	Pro
BMP3	Ser	...	Ala	...	Gln
GDF-1	...	Asn	Gln	...	Gln
60A	...	Phe	Ser	Asn
BMP5	...	Phe	Asp	Ser
BMP6	...	Asn	Asp	Ser
				30					35

46

hOP-1	Phe	Pro	Leu	Asn	Ser	Tyr	Met	Asn	Ala
mOP-1
hOP-2	Asp	...	Cys
mOP-2	Asp	...	Cys
DPP	Ala	Asp	His	Phe	...	Ser
Vgl	Tyr	Thr	Glu	Ile	Leu	...	Gly
Vgr-1	Ala	His
CBMP-2A	Ala	Asp	His	Leu	...	Ser
CBMP-2B	Ala	Asp	His	Leu	...	Ser
GDF-1	Leu	...	Val	Ala	Leu	Ser	Gly	Ser**	...
BMP3	Met	Pro	Lys	Ser	Leu	Lys	Pro
60A	Ala	His
BMP5	Ala	His	Met
BMP6	Ala	His	Met

40

hOP-1	Thr	Asn	His	Ala	Ile	Val	Gln	Thr	Leu
mOP-1
hOP-2	Leu	...	Ser	...
mOP-2	Leu	...	Ser	...
DPP	Val
Vgl	Ser	Leu
Vgr-1
CBMP-2A
CBMP-2B
BMP3	Ser	Thr	Ile	...	Ser	Ile
GDF-1	Leu	Val	Leu	Arg	Ala	...
60A
BMP5
BMP6

45

50

hOP-1	Val	His	Phe	Ile	Asn	Pro	Glu	Thr	Val
mOP-1	Asp
hOP-2	...	His	Leu	Met	Lys	...	Asn	Ala	...
mOP-2	...	His	Leu	Met	Lys	...	Asp	Val	...
DPP	...	Asn	Asn	Asn	Gly	Lys	...
Vgl	Ser	...	Glu	Asp	Ile
Vgr-1	Val	Met	Tyr	...
CBMP-2A	...	Asn	Ser	Val	...	Ser	---	Lys	Ile
CBMP-2B	...	Asn	Ser	Val	...	Ser	---	Ser	Ile
BMP3	...	Arg	Ala**	Gly	Val	Val	Pro	Gly	Ile
GDF-1	Met	...	Ala	Ala	Ala	...	Gly	Ala	Ala
60A	Leu	Leu	Glu	...	Lys	Lys	...
BMP5	Leu	Met	Phe	...	Asp	His	...
BMP6	Leu	Met	Tyr	...
		55					60		

hOP-1	Pro	Lys	Pro	Cys	Cys	Ala	Pro	Thr	Gln
mOP-1
hOP-2	Ala	Lys
mOP-2	Ala	Lys
DPP	Ala	Val
Vgl	...	Leu	Val	Lys
Vgr-1	Lys
CBMP-2A	Ala	Val	Glu
CBMP-2B	Ala	Val	Glu
BMP3	...	Glu	Val	...	Glu	Lys
GDF-1	Asp	Leu	Val	...	Ala	Arg
60A	Arg
BMP5	Lys
BMP6	Lys
			65					70	

48

hOP-1	Leu	Asn	Ala	Ile	Ser	Val	Leu	Tyr	Phe
mOP-1
hOP-2	...	Ser	...	Thr	Tyr
mOP-2	...	Ser	...	Thr	Tyr
Vgl	Met	Ser	Pro	Met	...	Phe	Tyr
Vgr-1	Val
DPP	...	Asp	Ser	Val	Ala	Met	Leu
CBMP-2A	...	Ser	Met	Leu
CBMP-2B	...	Ser	Met	Leu
BMP3	Met	Ser	Ser	Leu	...	Ile	...	Phe	Tyr
GDF-1	...	Ser	Pro	Phe	...
60A	...	Gly	...	Leu	Pro	His
BMP5
BMP6

75

80

hOP-1	Asp	Asp	Ser	Ser	Asn	Val	Ile	Leu	Lys
mOP-1
hOP-2	...	Ser	...	Asn	Arg
mOP-2	...	Ser	...	Asn	Arg
DPP	Asn	...	Gln	...	Thr	...	Val
Vgl	...	Asn	Asn	Asp	Val	...	Arg
Vgr-1	Asn
CBMP-2A	...	Glu	Asn	Glu	Lys	...	Val
CBMP-2B	...	Glu	Tyr	Asp	Lys	...	Val
BMP3	...	Glu	Asn	Lys	Val
GDF-1	...	Asn	...	Asp	Val	...	Arg
60A	Leu	Asn	Asp	Glu	Asn
BMP5
BMP6	Asn

85

hOP-1	Lys	Tyr	Arg	Asn	Met	Val	Val	Arg
mOP-1
hOP-2	...	His	Lys
mOP-2	...	His	Lys
DPP	Asn	...	Gln	Glu	...	Thr	...	Val
Vgl	His	...	Glu	Ala	...	Asp
Vgr-1
CBMP-2A	Asn	...	Gln	Asp	Glu
CBMP-2B	Asn	...	Gln	Glu	Glu
BMP3	Val	...	Pro	Thr	...	Glu
GDF-1	Gln	...	Glu	Asp	Asp
60A	Ile	...	Lys
BMP5
BMP6	Trp
	90					95		

hOP-1	Ala	Cys	Gly	Cys	His
mOP-1
hOP-2
mOP-2
DPP	Gly	Arg
Vgl	Glu	Arg
Vgr-1
CBMP-2A	Gly	Arg
CBMP-2B	Gly	Arg
BMP3	Ser	...	Ala	...	Arg
GDF-1	Glu	Arg
60A	Ser
BMP5	Ser
BMP6

****Between residues 56 and 57 of BMP3 is a Val residue;
between residues 43 and 44 of GDF-1 lies
the amino acid sequence Gly-Gly-Pro-Pro.**

As is apparent from the foregoing amino acid sequence comparisons, significant amino acid changes can be made within the generic sequences while retaining the morphogenic activity. For example, while the GDF-1 protein sequence depicted in Table II shares only about 50% amino acid identity with the hOP1 sequence described therein, the GDF-1 sequence shares greater than 70% amino acid sequence homology (or "similarity") with the hOP1 sequence, where "homology" or "similarity" includes allowed conservative amino acid changes within the sequence as defined by Dayoff, et al., Atlas of Protein Sequence and Structure vol.5, supp.3, pp.345-362, (M.O. Dayoff, ed., Nat'l BioMed. Res. Fd'n, Washington D.C. 1979.)

The currently most preferred protein sequences detectable as morphogens in this invention include those having greater than 60% identity, preferably greater than 65% identity, with the amino acid sequence defining the conserved six cysteine skeleton of hOP1 (e.g., residues 43-139 of Seq. ID No. 5). These most preferred sequences include both allelic and species variants of the OP-1 and OP-2 proteins, including the *Drosophila* 60A protein. Accordingly, in still another preferred aspect, the invention includes detection of morphogens comprising species of polypeptide chains having the generic amino acid sequence referred to herein as "OPX", which defines the seven cysteine skeleton and accommodates the identities between the various identified mouse and human OP1 and OP2 proteins. OPX is presented in Seq. ID No. 29. As described therein, each Xaa at a given position

independently is selected from the residues occurring at the corresponding position in the C-terminal sequence of mouse or human OP1 or OP2 (see Seq. ID Nos. 5-8 and/or Seq. ID Nos. 16-23).

3. Tissue-Specific Expression of OP-1

Once a morphogen is identified in a tissue, its level may be determined either at the protein or nucleic acid level. By comparing the levels of production of a given morphogen among different tissues, it is possible to determine the tissue(s) of origin of that morphogen. The level of production of the morphogen OP-1 in different tissues is one example of a morphogen having a tissue of origin, i.e., the kidney, which contains a cell type that can also be used as the cell type which is used to screen, according to the invention, different compounds for their potential effects on morphogen (OP-1) production.

The level of OP-1 varies among different tissue types. In order to screen compounds for their effect on the production of OP-1 by a given cell type, it may be desirable to determine which tissues produce levels of OP-1 which are sufficiently high to show a potential decrease and sufficiently low to show a potential increase in production. Different tissues may be screened at the RNA level as follows.

Any probe capable of hybridizing specifically to a transcript, and distinguishing the transcript of interest from other, related transcripts may be used. Because the morphogens to be detected in the methods of this invention share such high sequence homology in their C-terminal domain, the tissue distribution of a specific morphogen transcript may best be determined using a probe specific

for the "pro" region of the immature protein and/or the N-terminal heterogeneous region of the mature protein. Another useful probe sequence is the 3' non-coding region immediately following the stop codon. These portions of the sequence vary substantially among the morphogens of this invention, and accordingly, are specific for each protein. For example, a particularly useful Vgr-1-specific probe sequence is the PvuII-SacI fragment, a 265 bp fragment encoding both a portion of the pro region and the N-terminus of the mature sequence. Similarly, particularly useful mOP-1-specific probe sequences are the BstXI-BglI fragment, a 0.68kb sequence that covers approximately two-thirds of the mOP1 pro region; a StuI-StuI fragment, a 0.2 kb sequence immediately upstream of the 7-cysteine domain, and an EarI-PstI fragment, a 0.3kb fragment containing the 3'untranslated sequence. Similar approaches may be used, for example, with hOP-1 (SEQ. ID NO.16) or human or mouse OP-2 (SEQ. ID NOS.20 and 22).

Using morphogen-specific oligonucleotide probes, morphogen transcripts can be identified in mammalian tissues, using standard methodologies well known to those having ordinary skill in the art. Briefly, total RNA from mouse embryos and organs from post-natal animals is prepared using the acid guanidine thiocyanate-phenol-chloroform method (Chomczynski et al., Anal. Biochem. 162:156-159, 1987). The RNA may be dissolved in TES buffer (10 mM Tris-HCl, 1 mM EDTA, 0.1% SDS, pH 7.5) and treated with Proteinase K (approx. 1.5 mg per g tissue sample) at 45°C for 1 hr. Poly(A)⁺ RNA selection on oligo(dT)-cellulose (Type 7, Pharmacia LKB Biotechnology Inc., Piscataway, NJ) may be done in a batch procedure by mixing 0.1 g oligo(dT)-cellulose with 11 ml RNA solution (from 1 g

tissue) in TES buffer and 0.5 M NaCl). Thereafter the oligo(dT) cellulose is washed in binding buffer (0.5 M NaCl, 10 mM Tris-HCl, 1 mM EDTA, pH 7.5) and poly(A)⁺ RNA is eluted with water. Poly(A)⁺ RNA (5 or 15 µg/lane) is fractionated on 1 or 1.2% agarose-formaldehyde gels (Selden, in Current Protocols in Molecular Biology, Ausubel et al. eds., pp. 1-4, 8, 9, Greene Publishing and Wiley-Interscience, New York, 1991). 1 µl of 400 µg/ml ethidium bromide is added to each sample prior to heat denaturation (Rosen et al., Focus 12:23-24, 1990). Following electrophoresis, the gels are photographed and the RNA is blotted overnight onto Nytran nitrocellulose membranes (Schleicher & Schuell Inc., Keene, NH) with 10 x SSC. The membranes are baked at 80°C for 30-60 min. and irradiated with UV light (1 mW/cm² for 25 sec.). The Northern hybridization conditions may be as previously described (Ozkaynak et al., EMBO J. 9:2085-2093, 1990). For re-use, the filters may be deprobed in 1 mM Tris-HCl, 1 mM EDTA, 0.1% SDS, pH 7.5, at 90-95°C and exposed to film to assure complete removal of previous hybridization signals.

One probe which may be used to screen for transcripts encoding a morphogen includes a portion of or the complete OP-1 cDNA, which may be used to detect the presence of OP-1 mRNA or mRNAs of related morphogens. The sequence of the murine cDNA gene is set forth in SEQ ID NO:14.

OP-1 mRNA expression was analyzed in 17 day mouse embryos and 3 day post-natal mice by sequentially hybridizing filters with various probes. Probes from regions other than the highly conserved 7-cysteine domain were selected because this region is highly variable among

members of the TGF- β superfamily. Fig. 1 shows the fragments of OP-1, used as probes in the Northern hybridizations. The solid box indicates the putative signal peptide and the hatched box corresponds to the TGF- β -like domain that contains the seven cysteine residues. Asterisks indicate the potential N-glycosylation sites. The arrow marks the location of the cleavage site for OP-1 maturation. Three solid bars below the diagram indicate the OP-1 specific fragments used in making 32 P-labeled probes (0.68 kb BstXI - BglI fragment, 0.20 kb StuI - StuI fragment and 0.34 kb EarI - PstI non-coding fragment).

Hybridization with a probe that covers approximately two thirds of the pro region (the 0.68 kb BstXI-BglI fragment), reveals a 4 kb message and 3 messages at 1.8 kb, 2.2 kb and 2.4 kb (Fig. 2B and D, and Fig. 3). In the Northern hybridization of Fig. 2, equal amounts (15 μ g) of poly(A)⁺ RNA were loaded into each lane, electrophoresed on a 1% agarose-formaldehyde gel, blotted and hybridized. A 0.24 - 9.49 kb RNA ladder (Bethesda Research Labs, Inc.) was used as size standard. The same filter was used for sequential hybridizations with labeled probes specific for OP-1 (Panels B and D), Vgr-1 (Panel C), and EF-Tu (Panel A). Panel A: the EF-Tu specific probe (a control) was the 0.4 kb HindIII-SacI fragment (part of the coding region), the SacI site used belonged to the vector; Panel B: the OP-1 specific probe was the 0.68 kb BstXI-BglI fragment (two thirds of the pro region and upstream sequences of the mature domain, not including any sequences from the 7-cysteine domain); Panel C: the Vgr-1 specific probe was the 0.26 kb PvuII-SacI fragment (part of the pro region and the amino-terminal sequences of the mature

domain, including the first cysteine) (Lyons et al., 1989, Proc. Nat. Aca. Sci. 86: 4554, hereby incorporated by reference). Panel D: the OP-1 (3' flanking) specific probe was the 0.34 kb *Eco*I-*Pst*I fragment (3' untranslated sequences immediately following the sequences encoding OP-1).

In Fig. 3, the tissues to be used for RNA preparation were obtained from two week old mice (Panel A) or 5 week old mice (Panel B), with the exception of poly A+ RNA which was obtained from kidney adrenal gland of two week old mice (Panel B). Equal amounts of poly A+ RNA (15 μ g for Panel A and 5 μ g for Panel B) were loaded into each well. After electrophoresis (1.2% agarose-formaldehyde gels) and blotting, RNA was hybridized to the OP-1 specific 3' flanking probe described in the legend of Fig. 2 (Panel D). The 0.24-9.5 kb RNA ladder was used as size standard. The arrowheads indicate the OP-1 specific messages. The lower section of Panels A and B show the hybridization pattern obtained with the EF-Tu specific probe (a control).

Although the size of the Vgr-1 specific message is close to the 4 kb OP-1 species (Fig. 2 Panel C), the OP-1 4 kb mRNA is somewhat larger. To further rule out cross-hybridization with a non-OP-1 message, the 0.2 kb *Stu*I-*Stu*I fragment which represents the gene specific sequences immediately upstream of those encoding the 7-cysteine domain was used. This probe gave a hybridization pattern similar to the one shown in Fig. 2 Panel B (data not shown). A third probe, the 0.34 kb *Eco*I-*Pst*I fragment containing 3' untranslated sequences, also confirmed the pattern (Fig. 2 Panel D). Thus, the same four OP-1 specific messages were observed with three distinct probes.

The appearance of a new 4 kb OP-1 mRNA species was initially interpreted as cross hybridization of the OP-1 probe with Vgr-1 mRNA, which is approximately this size (Fig. 2 Panel C). However, the 4 kb message was detected with three different OP-1 specific probes, including one specific to the 3' untranslated region, and moreover it was separated from Vgr-1 message on the basis of size. Most likely, therefore, the 4 kb mRNA (and the three species of 1.8 kb, 2.2 kb and 2.4 kb) results from alternative splicing of OP-1 transcripts. The 4 kb OP-1 mRNA could also represent a bicistronic mRNA. The 4 kb message is a minor species in kidney, while it is more prominent in adrenal tissue.

The level of OP-1 expression was compared in different tissues using poly(A)⁺ RNA prepared from brain, spleen, lung, kidney and adrenal gland, heart, and liver of 13 day post-natal mice. The RNA was analyzed on Northern blots by hybridization to various probes (Fig. 3. Equal amounts of mRNA, as judged by optical density, were fractionated on agarose formaldehyde gels. Ethidium bromide staining of the gels revealed some residual ribosomal RNA in addition to the mRNA and provided another assurance that the mRNA was not degraded and that there was not significant quantitative or qualitative variation in the preparation. As control for mRNA recovery, EF-Tu (translational elongation factor) mRNA was probed (assuming uniform expression of EF-Tu in most tissues). A great variation in the level of OP-1 expression was observed in spleen, lung, kidney and adrenal tissues whereas EF-Tu mRNA levels appeared relatively constant in these tissues (Fig. 3 Panel A). The highest level of OP-1 mRNA was found in the kidneys. Uniformly lower levels of EF-Tu mRNA were

found in brain, heart and liver (Fig. 3 Panel A). Additional analysis of OP-1 mRNA showed the presence of significant amounts of OP-1 mRNA in the bladder (data not shown). In summary, next to kidney, bladder and adrenal tissue, brain tissue contained the highest levels of OP-1 RNA, whereas heart and liver did not give detectable signals.

OP-1 mRNA patterns display qualitative changes in the various tissues. Of the four messages found in brain, the 2.2 kb message is most abundant whereas in lung and spleen the 1.8 kb message predominates. Levels of the 1.8-2.4 kb in the kidney OP-1 mRNA are approximately two times higher in 3 day post-natal mice than in 17 day embryos, perhaps reflecting phases in bone and/or kidney development. mRNA was also prepared from carefully separated renal and adrenal tissues of 5 week old mice. Northern blot analysis (Figure 4, Panel B) revealed that the high levels of 2.2 kb mRNA were derived from renal tissue whereas the 4 kb mRNA was more prominent in adrenal tissue.

The detection of of OP-1 message primarily in the kidney but also in bladder links OP-1 expression specifically with the urinary tract. Interestingly, the related Vgr-1 is also expressed at significant levels in kidney although its main site of expression in lung.

Once the tissue-specific expression of a given morphogen is known, cell types known to exist in that tissue or cell lines derived from that tissue can be screened, in a similar manner, to identify the cell type within that tissue that is actually responsible for the tissue specific synthesis and secretion of the morphogen. Once a cell type which produces the morphogen in an amount

sufficient to detect increases or decreases in the production level of the morphogen upon exposure to a compound is identified, it may be used in tissue culture assay to rapidly screen for the ability of compound to upregulate or down regulate the synthesis and secretion of the morphogen. The level of morphogen production by the chosen cell type is determined with and without incubating the cell in culture with the compound, in order to assess the effects of the compound on the cell's ability to synthesize or secrete the morphogen. This can be accomplished by detection of the level of production of the morphogen either at the protein or mRNA level.

4. Growth of Cells in Culture

Cell cultures derived from kidney, adrenals, urinary bladder, brain, or other organs, may be prepared as described widely in the literature. For example, kidneys may be explanted from neonatal, new born, young or adult rodents (mouse or rat) and used in organ culture as whole or sliced (1-4 mm) tissues. Primary tissue cultures and established cell lines, also derived from kidney, adrenals, urinary, bladder, brain, or other tissues may be established in multiwell plates (6 well, 24 well, or 96 well) according to conventional cell culture techniques, and are cultured in the absence or presence of serum for a period of time (1-7 days). Cells may be cultured, for example, in Dulbecco's Modified Eagle medium (Gibco, Long Island, NY) containing serum (e.g., fetal calf serum at 1%-10%, Gibco) or in serum-deprived medium, as desired, or in defined medium (e.g., containing insulin, transferrin, glucose, albumin, or other growth factors).

Samples for testing the level of morphogen production include culture supernatants or cell lysates, collected periodically and evaluated for OP-1 production by immunoblot analysis of a portion of the cell culture itself, collected periodically and used to prepare polyA+ RNA for RNA analysis (Sambrook et al., eds., Molecular Cloning, 1989, Cold Spring Harbor Press, Cold Spring Harbor, NY). To monitor de novo OP-1 synthesis, some cultures are labeled with ^{35}S -methionine/ ^{35}S -cysteine mixture for 6-24 hours and then evaluated for morphogen production by conventional immunoprecipitation methods (Sambrook et al., eds., Molecular Cloning, 1989, Cold Spring Harbor Press, Cold Spring Harbor, NY). Alternatively, the production of morphogen or determination of the level of morphogen production may be ascertained using a simple assay for a parameter of cell growth, e.g., cellular proliferation or death. For example, where a morphogen is produced by a cultured cell line, the addition of antibody specific for the morphogen may result in relief from morphogen inhibition of cell growth. Thus, measurement of cellular proliferation can be used as an indication of morphogen production by a tissue.

5. Determination of Level of Morphogenic Protein

In order to quantitate the production of a morphogenic protein by a cell type, an immunoassay may be performed to detect the morphogen using a polyclonal or monoclonal antibody specific for that morphogen. For example, OP-1 may be detected using a polyclonal antibody specific for OP-1 in an ELISA, as follows.

1 $\mu\text{g}/100\text{ ul}$ of affinity-purified polyclonal rabbit IgG specific for OP-1 is added to each well of a 96-well

plate and incubated at 37°C for an hour. The wells are washed four times with 0.16M sodium borate buffer with 0.15 M NaCl (BSB), pH 8.2, containing 0.1% Tween 20. To minimize non-specific binding, the wells are blocked by filling completely with 1% bovine serum albumin (BSA) in BSB for 1 hour at 37°C. The wells are then washed four times with BSB containing 0.1% Tween 20. A 100 ul aliquot of an appropriate dilution of each of the test samples of cell culture supernatant is added to each well in triplicate and incubated at 37°C for 30 min. After incubation, 100 ul biotinylated rabbit anti-OP-1 serum (stock solution is about 1 mg/ml and diluted 1:400 in BSB containing 1% BSA before use) is added to each well and incubated at 37°C for 30 min. The wells are then washed four times with BSB containing 0.1% Tween 20. 100 ul streptavidin-alkaline (Southern Biotechnology Associates, Inc. Birmingham, Alabama, diluted 1:2000 in BSB containing 0.1% Tween 20 before use) is added to each well and incubated at 37°C for 30 min. The plates are washed four times with 0.5M Tris buffered Saline (TBS), pH 7.2. 50ul substrate (ELISA Amplification System Kit, Life Technologies, Inc., Bethesda, MD) are added to each well incubated at room temperature for 15 min. Then, 50 ul amplifier (from the same amplification system kit) is added and incubated for another 15 min at room temperature. The reaction is stopped by the addition of 50 ul 0.3 M sulphuric acid. The OD at 490 nm of the solution in each well is recorded. To quantitate OP-1 in culture media, a OP-1 standard curve is performed in parallel with the test samples.

6. Preparation of Polyclonal Antibody

Polyclonal antibody is prepared as follows. Each rabbit is given a primary immunization of 100 ug/500 ul E. coli-produced OP-1 monomer (amino acids 328-431 of SEQ. ID NO: 11) in 0.1% SDS mixed with 500 ul Complete Freund's Adjuvant. The antigen is injected subcutaneously at multiple sites on the back and flanks of the animal. The rabbit is boosted after a month in the same manner using incomplete Freund's Adjuvant. Test bleeds are taken from the ear vein seven days later. Two additional boosts and test bleeds are performed at monthly intervals until antibody against OP-1 is detected in the serum using an ELISA assay. Then, the rabbit is boosted monthly with 100 ug of antigen and bled (15 ml per bleed) at days seven and ten after boosting.

7. Preparation of Monoclonal Antibody and Neutralizing Monoclonal Antibody

Monoclonal antibody specific for a given morphogen may be prepared as follows. A mouse is given two injections of E. coli produced OP-1 monomer (amino acids 328-431 in SEQ ID NO:11). The first injection contains 100ug of OP-1 in complete Freund's adjuvant and is given subcutaneously. The second injection contains 50 ug of OP-1 in incomplete adjuvant and is given intraperitoneally. The mouse then receives a total of 230 ug of OP-1 (amino acids 307-431 of SEQ ID NO:11) in four intraperitoneal injections at various times over an eight month period. One week prior to fusion, The mouse is boosted intraperitoneally with 100 ug of OP-1 (15-139) and 30 ug of the N-terminal peptide (Ser293-Asn309-Cys) conjugated through the added cys residue to bovine serum albumin with

SMCC crosslinking agent. This boost is repeated five days (IP), four days (IP), three days (IP) and one day (IV) prior to fusion. The mouse spleen cells are then fused to myeloma (e.g., 653) cells at a ratio of 1:1 using PEG 1500 (Boehringer Mannheim), and the cell fusion is plated and screened for OP-1-specific antibodies using OP-1 (307-431) as antigen. The cell fusion and monoclonal screening are according to procedures widely available in the art. The neutralizing monoclonal is identified by its ability to block the biological activity of OP-1 when added to a cellular assay which responds biologically to added OP-1.

8. Identification of OP-1 Producing Cell Line Which Displays OP-1 Surface Receptors

During the process of routinely testing the effects of increasing concentrations of OP-1 and TGF- β on the proliferation of various cell lines, a cell line was identified which, surprising, appears not only to synthesize and secrete OP-1, but also to display cell surface receptors to which the secreted OP-1 binds and acts to inhibit proliferation of the cells. This cell line was identified after the following observations. Addition of increasing concentrations of OP-1 or TGF- β failed to increase or decrease the relatively low basal rate of proliferation of the cells. However, addition of a monoclonal antibody, which neutralizes the activity of Op-1, resulted in a large increase in the proliferation of the cells. In addition, simultaneous addition of the same quantity of OP-1 neutralizing monoclonal to a fixed amount of OP-1 resulted in an increase in proliferation which was intermediate between the low

basal level observed with OP-1 alone and the high level observed with the monoclonal alone. This cell line, which is an epithelial cell line that was derived from a bladder cell carcinoma, may be used in an assay of the invention. The parameter to be tested according to the invention is cellular proliferation. Thus, a compound(s) that increases or decreases the level of OP-1 production may be tested on this cell line as follows..

9. Assay for Identifying Drugs Which Affect OP-1 Synthesis

A simple medium flux screening assay can be configured in a standard 24 or 96 well microtiter dish, in which each well contains a constant number of a cell line having the characteristics described above. Increasing concentrations of an OP-1 neutralizing monoclonal antibody is added from left to right across the dish. A constant amount of different test substances is added from top to bottom on the dish. An increase in the synthesis and secretion of OP-1 (over its constitutive (non-induced) level) will be indicated by an increase in the amount of OP-1 neutralizing antibody required to release the cells from the antimitogenic activity of OP-1. A decrease in the synthesis and secretion of OP-1 (below its constitutive (repressed) level) will be indicated by the observation that decreased concentrations of the OP-1 neutralizing monoclonal antibody will be required to release the cells from the antimitogenic activity of OP-1. One of the major advantages of this assay is that the end point, i.e., the dilution of antibody which has an effect on cell proliferation, is a measure of mitosis, or an increase in

the number of cells per well. Because several convenient and rapid assays exist for quantitating cell numbers, this assay is faster and requires significantly fewer steps to perform.

The assay may be performed as follows. After addition of appropriate concentrations of the OP-1 neutralizing monoclonal antibody and test substances to the wells containing the cells, the dishes are placed in an incubator at 37°C for a period of 1-3 days. After completion of incubation/growth period, the dishes are removed and the cells in the individual wells are washed and stained with a vital stain, such as crystal violet. Washing and staining procedures are well-known in the art. The cells are then lysed and the stain dissolved in a constant amount of a solvent, such as ethanol. Quantitations of the dissolved stain, which is readily performed on an automated plate vendor, allows for direct quantitation of the number of cells in each well.

The above-described assay has the advantages of being rapid and easy to perform because it requires few steps. Another advantage is intrinsic to the assay; drugs which are screened according to this procedure that result in cell death (i.e., cytotoxic substances) are immediately, identifiable without the need of operator observation. In addition, although drugs that stop the growth of the cells (i.e., cytostatic substances) are scored as positive due to failure to see increases in cell numbers, they are automatically scored as suspect due to the failure of the highest concentrations of OP-1 neutralizing monoclonal antibody to release the cells from the antimitogenic activity of OP-1.

10. Candidate Drugs to Screen

The screening methods of the invention is used to test compounds for their effect on the production of morphogenic protein by a given cell type. Examples of compounds which may be screened include but are not limited to chemicals, biological response modifiers (e.g., lymphokines, cytokines, hormones, or vitamins), plant extracts, microbial broths and extracts medium conditioned by eukaryotic cells, body fluids, or tissue extracts.

The invention may be embodied in other specific forms without departing from the spirit or essential characteristics thereof. The present embodiments are therefore to be considered in all respects as illustrative and not restrictive, the scope of the invention being indicated by the appended claims rather than by the foregoing description, and all changes which come within the meaning and range of equivalency of the claims are therefore intended to be embraced therein.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: John Smart
Herman Oppermann
Engin Ozkaynak
Thangavel Kuberasampath
David C. Rueger
Roy H.L. Pang
Charles M. Cohen
- (ii) TITLE OF INVENTION: MORPHOGENIC
PROTEIN SCREENING METHOD
- (iii) NUMBER OF SEQUENCES: 33
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Creative BioMolecules
 - (B) STREET: 35 South Street
 - (C) CITY: Hopkinton
 - (D) STATE: Massachusetts
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 01748
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette, 5.25,
360kb storage
 - (B) COMPUTER: IBM XT
 - (C) OPERATING SYSTEM: DOS 3.30
 - (D) SOFTWARE: ASC II TEXT
- (vi) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 667,274
 - (B) FILING DATE: March 11, 1991
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 752,861
 - (B) FILING DATE: AUGUST 30, 1991

(viii) ATTORNEY/AGENT INFORMATION

(A) NAME: PITCHER, EDMUND R.

(B) REG. NO.: 27,829

(C) DOCKET NO.: CRP-058^c_kPC

(ix) TELEPHONE:

(A) 617/248-7000

(B) TELEFAX: 617/248-7100

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acids

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) **FEATURE:**

(A) NAME: Generic Sequence 1

(D) OTHER INFORMATION: Each Xaa indicates one of the 20 naturally-occurring L-isomer, α -amino acids or a derivative thereof.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

[illegible]

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acids

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) **FEATURE:**

(A) NAME: Generic Sequence 2

(D) OTHER INFORMATION: Each Xaa indicates one of the 20 naturally-occurring L-isomer, α -amino acids or a derivative thereof.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acids

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME: Generic Sequence 3

(D) OTHER INFORMATION: wherein each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

      Leu Tyr Val Xaa Phe
        1             5
Xaa Xaa Xaa Gly Trp Xaa Xaa Trp Xaa
          10
Xaa Ala Pro Gly Xaa Xaa Xaa Ala
  15             20
Xaa Tyr Cys Xaa Gly Xaa Cys Xaa
      25             30
Xaa Pro Xaa Xaa Xaa Xaa Xaa
          35
Xaa Xaa Xaa Asn His Ala Xaa Xaa
      40             45
Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa
          50
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
      55             60
Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa
          65

```

```

Xaa Xaa Xaa Leu Xaa Xaa Xaa
 70                               75
Xaa Xaa Xaa Xaa Val Xaa Leu Xaa
                        80
Xaa Xaa Xaa Xaa Met Xaa Val Xaa
 85                               90
Xaa Cys Gly Cys Xaa
                        95

```

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acids
 - (C) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME: Generic Sequence 4
 - (D) OTHER INFORMATION: wherein each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Cys Xaa Xaa Xaa Xaa Leu Tyr Val Xaa Phe
 1                               5                               10
Xaa Xaa Xaa Gly Trp Xaa Xaa Trp Xaa
                        15
Xaa Ala Pro Xaa Gly Xaa Xaa Ala
 20                               25
Xaa Tyr Cys Xaa Gly Xaa Cys Xaa
                        30                               35
Xaa Pro Xaa Xaa Xaa Xaa Xaa
                        40

```

```

Asn Xaa Xaa Asn His Ala Xaa Xaa
      45                      50
Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa
      55
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
      60                      65
Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa
      70
Xaa Xaa Xaa Leu Xaa Xaa Xaa
      75                      80
Xaa Xaa Xaa Xaa Val Xaa Leu Xaa
      85
Xaa Xaa Xaa Xaa Met Xaa Val Xaa
      90                      95
Xaa Cys Gly Cys Xaa
      100

```

- (2) INFORMATION FOR SEQ ID NO:5:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 139 amino acids
 - (B) TYPE: amino acids
 - (C) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (ix) FEATURE:
 - (A) NAME: hOP-1 (mature form)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

Ser  Thr  Gly  Ser  Lys  Gln  Arg  Ser  Gln
  1                      5
Asn  Arg  Ser  Lys  Thr  Pro  Lys  Asn  Gln
 10                      15
Glu  Ala  Leu  Arg  Met  Ala  Asn  Val  Ala
    20                      25
Glu  Asn  Ser  Ser  Ser  Asp  Gln  Arg  Gln
    30                      35

```

Ala	Cys	Lys	Lys	His	Glu	Leu	Tyr	Val
			40					45
Ser	Phe	Arg	Asp	Leu	Gly	Trp	Gln	Asp
			50					
Trp	Ile	Ile	Ala	Pro	Glu	Gly	Tyr	Ala
55					60			
Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ala
	65					70		
Phe	Pro	Leu	Asn	Ser	Tyr	Met	Asn	Ala
		75					80	
Thr	Asn	His	Ala	Ile	Val	Gln	Thr	Leu
			85					90
Val	His	Phe	Ile	Asn	Pro	Glu	Thr	Val
			95					
Pro	Lys	Pro	Cys	Cys	Ala	Pro	Thr	Gln
100					105			
Leu	Asn	Ala	Ile	Ser	Val	Leu	Tyr	Phe
	110					115		
Asp	Asp	Ser	Ser	Asn	Val	Ile	Leu	Lys
		120					125	
Lys	Tyr	Arg	Asn	Met	Val	Val	Arg	Ala
			130					135
Cys	Gly	Cys	His					

- (2) INFORMATION FOR SEQ ID NO:6:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acids
- (C) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
- (A) NAME: mOP-1 (mature form)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ser	Thr	Gly	Gly	Lys	Gln	Arg	Ser	Gln
1				5				
Asn	Arg	Ser	Lys	Thr	Pro	Lys	Asn	Gln
10					15			
Glu	Ala	Leu	Arg	Met	Ala	Ser	Val	Ala
	20					25		
Glu	Asn	Ser	Ser	Ser	Asp	Gln	Arg	Gln
		30					35	
Ala	Cys	Lys	Lys	His	Glu	Leu	Tyr	Val
			40					45
Ser	Phe	Arg	Asp	Leu	Gly	Trp	Gln	Asp
				50				
Trp	Ile	Ile	Ala	Pro	Glu	Gly	Tyr	Ala
55					60			
Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ala
	65					70		
Phe	Pro	Leu	Asn	Ser	Tyr	Met	Asn	Ala
		75					80	
Thr	Asn	His	Ala	Ile	Val	Gln	Thr	Leu
			85					90
Val	His	Phe	Ile	Asn	Pro	Asp	Thr	Val
				95				
Pro	Lys	Pro	Cys	Cys	Ala	Pro	Thr	Gln
100					105			
Leu	Asn	Ala	Ile	Ser	Val	Leu	Tyr	Phe
	110							115

Asp	Asp	Ser	Ser	Asn	Val	Ile	Leu	Lys
		120					125	
Lys	Tyr	Arg	Asn	Met	Val	Val	Arg	Ala
			130					135
Cys	Gly	Cys	His					

- (2) INFORMATION FOR SEQ ID NO:7:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 139 amino acids
 - (B) TYPE: amino acids
 - (C) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (ix) FEATURE:
 - (A) NAME: hOP-2 (mature form)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ala	Val	Arg	Pro	Leu	Arg	Arg	Arg	Gln
1				5				
Pro	Lys	Lys	Ser	Asn	Glu	Leu	Pro	Gln
10					15			
Ala	Asn	Arg	Leu	Pro	Gly	Ile	Phe	Asp
20						25		
Asp	Val	His	Gly	Ser	His	Gly	Arg	Gln
		30					35	
Val	Cys	Arg	Arg	His	Glu	Leu	Tyr	Val
			40					45
Ser	Phe	Gln	Asp	Leu	Gly	Trp	Leu	Asp
				50				
Trp	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser
55					60			
Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ser
65						70		
Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	Ala
		75					80	
Thr	Asn	His	Ala	Ile	Leu	Gln	Ser	Leu
			85					90

Val	His	Leu	Met	Lys	Pro	Asn	Ala	Val
				95				
Pro	Lys	Ala	Cys	Cys	Ala	Pro	Thr	Lys
100					105			
Leu	Ser	Ala	Thr	Ser	Val	Leu	Tyr	Tyr
	110					115		
Asp	Ser	Ser	Asn	Asn	Val	Ile	Leu	Arg
		120					125	
Lys	His	Arg	Asn	Met	Val	Val	Lys	Ala
			130					135
Cys	Gly	Cys	His					

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acids

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME: mOP-2 (mature form)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ala	Ala	Arg	Pro	Leu	Lys	Arg	Arg	Gln
1				5				
Pro	Lys	Lys	Thr	Asn	Glu	Leu	Pro	His
10					15			
Pro	Asn	Lys	Leu	Pro	Gly	Ile	Phe	Asp
	20					25		
Asp	Gly	His	Gly	Ser	Arg	Gly	Arg	Glu
		30					35	
Val	Cys	Arg	Arg	His	Glu	Leu	Tyr	Val
			40					45
Ser	Phe	Arg	Asp	Leu	Gly	Trp	Leu	Asp
				50				
Trp	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser
55					60			

Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ala
	65					70		
Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	Ala
		75					80	
Thr	Asn	His	Ala	Ile	Leu	Gln	Ser	Leu
			85					90
Val	His	Leu	Met	Lys	Pro	Asp	Val	Val
				95				
Pro	Lys	Ala	Cys	Cys	Ala	Pro	Thr	Lys
100					105			
Leu	Ser	Ala	Thr	Ser	Val	Leu	Tyr	Tyr
	110					115		
Asp	Ser	Ser	Asn	Asn	Val	Ile	Leu	Arg
		120					125	
Lys	His	Arg	Asn	Met	Val	Val	Lys	Ala
			130					135
Cys	Gly	Cys	His					

- (2) INFORMATION FOR SEQ ID NO:9:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: amino acids
 - (C) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (ix) FEATURE:
 - (A) NAME: CBMP-2A(fx)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```

Cys Lys Arg His Pro Leu Tyr Val Asp Phe Ser
 1                      5                      10
Asp Val Gly Trp Asn Asp Trp Ile Val Ala Pro
          15                      20
Pro Gly Tyr His Ala Phe Tyr Cys His Gly Glu
          25                      30
Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser
          35                      40
Thr Asn His Ala Ile Val Gln Thr Leu Val Asn
          45                      50                      55
Ser Val Asn Ser Lys Ile Pro Lys Ala Cys Cys
          60                      65
Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu
          70                      75
Tyr Leu Asp Glu Asn Glu Lys Val Val Leu Lys
          80                      85
Asn Tyr Gln Asp Met Val Val Glu Gly Cys Gly
          90                      95
Cys Arg
100

```

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 amino acids

(B) TYPE: amino acids

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) **FEATURE:**

(A) NAME: CBMP-2B(fx)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

							Cys	Arg	Arg	His	Ser
							1				5
Leu	Tyr	Val	Asp	Phe	Ser	Asp	Val	Gly	Trp	Asn	
				10						15	
Asp	Trp	Ile	Val	Ala	Pro	Pro	Gly	Tyr	Gln	Ala	
			20						25		
Phe	Tyr	Cys	His	Gly	Asp	Cys	Pro	Phe	Pro	Leu	
		30						35			
Ala	Asp	His	Leu	Asn	Ser	Thr	Asn	His	Ala	Ile	
	40					45					
Val	Gln	Thr	Leu	Val	Asn	Ser	Val	Asn	Ser	Ser	
50					55					60	
Ile	Pro	Lys	Ala	Cys	Cys	Val	Pro	Thr	Glu	Leu	
				65						70	
Ser	Ala	Ile	Ser	Met	Leu	Tyr	Leu	Asp	Glu	Tyr	
			75						80		
Asp	Lys	Val	Val	Leu	Lys	Asn	Tyr	Gln	Glu	Met	
		85							90		
Val	Val	Glu	Gly	Cys	Gly	Cys	Arg				
	95					100					

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acids

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) **FEATURE:**

(A) NAME: DPP(fx)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

[illegible]

- (2) INFORMATION FOR SEQ ID NO:12:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acids
 - (C) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (ix) FEATURE:
 - (A) NAME: Vgl(fx)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```

Cys Lys Lys Arg His Leu Tyr Val Glu Phe Lys
 1                   5                   10
Asp Val Gly Trp Gln Asn Trp Val Ile Ala Pro
          15                   20
Gln Gly Tyr Met Ala Asn Tyr Cys Tyr Gly Glu
          25                   30
Cys Pro Tyr Pro Leu Thr Glu Ile Leu Asn Gly
          35                   40
Ser Asn His Ala Ile Leu Gln Thr Leu Val His
          45                   50                   55
Ser Ile Glu Pro Glu Asp Ile Pro Leu Pro Cys
          60                   65
Cys Val Pro Thr Lys Met Ser Pro Ile Ser Met
          70                   75
Leu Phe Tyr Asp Asn Asn Asp Asn Val Val Leu
          80                   85
Arg His Tyr Glu Asn Met Ala Val Asp Glu Cys
          90                   95
Gly Cys Arg
100

```

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acids

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) **FEATURE:**

(A) NAME: Vgr-1(fx)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

[illegible]

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 106 amino acids
 (B) TYPE: protein
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: human
(F) TISSUE TYPE: BRAIN

```
(ix) FEATURE:
(D) OTHER INFORMATION:
    /product= "GDF-1 (fx)"
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

[illegible]

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Cys Xaa Xaa Xaa Xaa
 1 5

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1822 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: HOMO SAPIENS
 (F) TISSUE TYPE: HIPPOCAMPUS

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 49..1341
 (D) OTHER INFORMATION: /standard_name= "hOP1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGTGCGGGCC CGGAGCCCGG AGCCCGGGTA GCGCGTAGAG CCGGCGCG ATG CAC GTG	57
Met His Val	
1	
CGC TCA CTG CGA GCT GCG GCG CCG CAC AGC TTC GTG GCG CTC TGG GCA	105
Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala	
5 10 15	
CCC CTG TTC CTG CTG CGC TCC GCC CTG GCC GAC TTC AGC CTG GAC AAC	153
Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn	
20 25 30 35	
GAG GTG CAC TCG AGC TTC ATC CAC CGG CGC CTC CGC AGC CAG GAG CGG	201
Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg	
40 45 50	
CGG GAG ATG CAG CGC GAG ATC CTC TCC ATT TTG GGC TTG CCC CAC CGC	249
Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg	
55 60 65	

CCG	CGC	CCG	CAC	CTC	CAG	GGC	AAG	CAC	AAC	TCG	GCA	CCC	ATG	TTC	ATG	297
Pro	Arg	Pro	His	Leu	Gln	Gly	Lys	His	Asn	Ser	Ala	Pro	Met	Phe	Met	
		70					75					80				
CTG	GAC	CTG	TAC	AAC	GCC	ATG	GCG	GTG	GAG	GAG	GGC	GGC	GGG	CCC	GGC	345
Leu	Asp	Leu	Tyr	Asn	Ala	Met	Ala	Val	Glu	Glu	Gly	Gly	Gly	Pro	Gly	
	85					90					95					
GGC	CAG	GGC	TTC	TCC	TAC	CCC	TAC	AAG	GCC	GTC	TTC	AGT	ACC	CAG	GGC	393
Gly	Gln	Gly	Phe	Ser	Tyr	Pro	Tyr	Lys	Ala	Val	Phe	Ser	Thr	Gln	Gly	
100					105					110					115	
CCC	CCT	CTG	GCC	AGC	CTG	CAA	GAT	AGC	CAT	TTC	CTC	ACC	GAC	GCC	GAC	441
Pro	Pro	Leu	Ala	Ser	Leu	Gln	Asp	Ser	His	Phe	Leu	Thr	Asp	Ala	Asp	
				120					125					130		
ATG	GTC	ATG	AGC	TTC	GTC	AAC	CTC	GTG	GAA	CAT	GAC	AAG	GAA	TTC	TTC	489
Met	Val	Met	Ser	Phe	Val	Asn	Leu	Val	Glu	His	Asp	Lys	Glu	Phe	Phe	
		135					140						145			
CAC	CCA	CGC	TAC	CAC	CAT	CGA	GAG	TTC	CGG	TTT	GAT	CTT	TCC	AAG	ATC	537
His	Pro	Arg	Tyr	His	His	Arg	Glu	Phe	Arg	Phe	Asp	Leu	Ser	Lys	Ile	
		150					155					160				
CCA	GAA	GGG	GAA	GCT	GTC	ACG	GCA	GCC	GAA	TTC	CGG	ATC	TAC	AAG	GAC	585
Pro	Glu	Gly	Glu	Ala	Val	Thr	Ala	Ala	Glu	Phe	Arg	Ile	Tyr	Lys	Asp	
	165					170					175					
TAC	ATC	CGG	GAA	CGC	TTC	GAC	AAT	GAG	ACG	TTC	CGG	ATC	AGC	GTT	TAT	633
Tyr	Ile	Arg	Glu	Arg	Phe	Asp	Asn	Glu	Thr	Phe	Arg	Ile	Ser	Val	Tyr	
180					185					190					195	
CAG	GTG	CTC	CAG	GAG	CAC	TTG	GGC	AGG	GAA	TCG	GAT	CTC	TTC	CTG	CTC	681
Gln	Val	Leu	Gln	Glu	His	Leu	Gly	Arg	Glu	Ser	Asp	Leu	Phe	Leu	Leu	
				200					205					210		
GAC	AGC	CGT	ACC	CTC	TGG	GCC	TCG	GAG	GAG	GGC	TGG	CTG	GTG	TTT	GAC	729
Asp	Ser	Arg	Thr	Leu	Trp	Ala	Ser	Glu	Glu	Gly	Trp	Leu	Val	Phe	Asp	
		215						220				225				
ATC	ACA	GCC	ACC	AGC	AAC	CAC	TGG	GTG	GTC	AAT	CCG	CGG	CAC	AAC	CTG	777
Ile	Thr	Ala	Thr	Ser	Asn	His	Trp	Val	Val	Asn	Pro	Arg	His	Asn	Leu	
		230					235					240				
GGC	CTG	CAG	CTC	TCG	GTG	GAG	ACG	CTG	GAT	GGG	CAG	AGC	ATC	AAC	CCC	825
Gly	Leu	Gln	Leu	Ser	Val	Glu	Thr	Leu	Asp	Gly	Gln	Ser	Ile	Asn	Pro	
	245					250					255					
AAG	TTG	GCG	GGC	CTG	ATT	GGG	CGG	CAC	GGG	CCC	CAG	AAC	AAG	CAG	CCC	873
Lys	Leu	Ala	Gly	Leu	Ile	Gly	Arg	His	Gly	Pro	Gln	Asn	Lys	Gln	Pro	
260					265					270					275	

TTC ATG GTG GCT TTC TTC AAG GCC ACG GAG GTC CAC TTC CGC AGC ATC Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe Arg Ser Ile 280 285 290	921
CGG TCC ACG GGG AGC AAA CAG CGC AGC CAG AAC CGC TCC AAG ACG CCC Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro 295 300 305	969
AAG AAC CAG GAA GCC CTG CGG ATG GCC AAC GTG GCA GAG AAC AGC AGC Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser 310 315 320	1017
AGC GAC CAG AGG CAG GCC TGT AAG AAG CAC GAG CTG TAT GTC AGC TTC Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe 325 330 335	1065
CGA GAC CTG GGC TGG CAG GAC TGG ATC ATC GCG CCT GAA GGC TAC GCC Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala 340 345 350 355	1113
GCC TAC TAC TGT GAG GGG GAG TGT GCC TTC CCT CTG AAC TCC TAC ATG Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met 360 365 370	1161
AAC GCC ACC AAC CAC GCC ATC GTG CAG ACG CTG GTC CAC TTC ATC AAC Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn 375 380 385	1209
CCG GAA ACG GTG CCC AAG CCC TGC TGT GCG CCC ACG CAG CTC AAT GCC Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala 390 395 400	1257
ATC TCC GTC CTC TAC TTC GAT GAC AGC TCC AAC GTC ATC CTG AAG AAA Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys 405 410 415	1305
TAC AGA AAC ATG GTG GTC CGG GCC TGT GGC TGC CAC TAGCTCCTCC Tyr Arg Asn Met Val Arg Ala Cys Gly Cys His 420 425 430	1351
GAGAATTCAG ACCCTTTGGG GCCAAGTTTT TCTGGATCCT CCATTGCTCG CCTTGGCCAG	1411
GAACCAGCAG ACCAACTGCC TTTTGTGAGA CCTTCCCCTC CCTATCCCCA ACTTTAAAGG	1471
TGTGAGAGTA TTAGGAAACA TGAGCAGCAT ATGGCTTTTG ATCAGTTTTT CAGTGGCAGC	1531
ATCCAATGAA CAAGATCCTA CAAGCTGTGC AGGCAAAACC TAGCAGGAAA AAAAAACAAC	1591
GCATAAAGAA AAATGGCCGG GCCAGGTCAT TGGCTGGGAA GTCTCAGCCA TGCACGGACT	1651
CGTTTCCAGA GGTAATTATG AGCGCCTACC AGCCAGGCCA CCCAGCCGTG GGAGGAAGGG	1711
GGCGTGGCAA GGGGTGGGCA CATTGGTGTC TGTGCGAAAG GAAAATTGAC CCGGAAGTTC	1771
CTGTAATAAA TGTACAATA AAACGAATGA ATGAAAAAAAA AAAAAAAAAA A	1822

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (D) OTHER INFORMATION: /Product="OP1-PP"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```

Met His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala
 1             5             10             15
Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser
      20             25             30
Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser
      35             40             45
Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu
      50             55             60
Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro
      65             70             75             80
Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly
      85             90             95
Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser
      100            105            110
Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr
      115            120            125
Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys
      130            135            140
Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu
      145            150            155            160
Ser Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile
      165            170            175
Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile
      180            185            190
Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu
      195            200            205

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Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu
 210 215 220
 Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg
 225 230 235 240
 His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser
 245 250 255
 Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn
 260 265 270
 Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe
 275 280 285
 Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser
 290 295 300
 Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu
 305 310 315 320
 Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr
 325 330 335
 Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu
 340 345 350
 Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn
 355 360 365
 Ser Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His
 370 375 380
 Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln
 385 390 395 400
 Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile
 405 410 415
 Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
 420 425 430

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1873 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: MURIDAE
- (F) TISSUE TYPE: EMBRYO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 104..1393
- (D) OTHER INFORMATION: /note= "MOP1 (CDNA)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTGCAGCAAG TGACCTCGGG TCGTGGACCG CTGCCCTGCC CCCTCCGCTG CCACCTGGGG	60
CGGCGCGGGC CCGGTGCCCC GGATCGCGCG TAGAGCCGGC GCG ATG CAC GTG CGC	115
Met His Val Arg	
1	
TCG CTG CGC GCT GCG GCG CCA CAC AGC TTC GTG GCG CTC TGG GCG CCT	163
Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala Pro	
5 10 15 20	
CTG TTC TTG CTG CGC TCC GCC CTG GCC GAT TTC AGC CTG GAC AAC GAG	211
Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn Glu	
25 30 35	
GTG CAC TCC AGC TTC ATC CAC CGG CGC CTC CGC AGC CAG GAG CGG CGG	259
Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg Arg	
40 45 50	
GAG ATG CAG CGG GAG ATC CTG TCC ATC TTA GGG TTG CCC CAT CGC CCG	307
Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg Pro	
55 60 65	
CGC CCG CAC CTC CAG GGA AAG CAT AAT TCG GCG CCC ATG TTC ATG TTG	355
Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met Leu	
70 75 80	
GAC CTG TAC AAC GCC ATG GCG GTG GAG GAG AGC GGG CCG GAC GGA CAG	403
Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Ser Gly Pro Asp Gly Gln	
85 90 95 100	

GGC TTC TCC TAC CCC TAC AAG GCC GTC TTC AGT ACC CAG GGC CCC CCT Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly Pro Pro 105 110 115	451
TTA GCC AGC CTG CAG GAC AGC CAT TTC CTC ACT GAC GCC GAC ATG GTC Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp Ala Asp Met Val 120 125 130	499
ATG AGC TTC GTC AAC CTA GTG GAA CAT GAC AAA GAA TTC TTC CAC CCT Met Ser Phe Val Asn Leu Val Glu His Asp Lys Glu Phe Phe His Pro 135 140 145	547
CGA TAC CAC CAT CGG GAG TTC CGG TTT GAT CTT TCC AAG ATC CCC GAG Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser Lys Ile Pro Glu 150 155 160	595
GGC GAA CGG GTG ACC GCA GCC GAA TTC AGG ATC TAT AAG GAC TAC ATC Gly Glu Arg Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp Tyr Ile 165 170 175 180	643
CGG GAG CGA TTT GAC AAC GAG ACC TTC CAG ATC ACA GTC TAT CAG GTG Arg Glu Arg Phe Asp Asn Glu Thr Phe Gln Ile Thr Val Tyr Gln Val 185 190 195	691
CTC CAG GAG CAC TCA GGC AGG GAG TCG GAC CTC TTC TTG CTG GAC AGC Leu Gln Glu His Ser Gly Arg Glu Ser Asp Leu Phe Leu Leu Asp Ser 200 205 210	739
CGC ACC ATC TGG GCT TCT GAG GAG GGC TGG TTG GTG TTT GAT ATC ACA Arg Thr Ile Trp Ala Ser Glu Glu Gly Trp Leu Val Phe Asp Ile Thr 215 220 225	787
GCC ACC AGC AAC CAC TGG GTG GTC AAC CCT CGG CAC AAC CTG GGC TTA Ala Thr Ser Asn His Trp Val Val Asn Pro Arg His Asn Leu Gly Leu 230 235 240	835
CAG CTC TCT GTG GAG ACC CTG GAT GGG CAG AGC ATC AAC CCC AAG TTG Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile Asn Pro Lys Leu 245 250 255 260	883
GCA GGC CTG ATT GGA CGG CAT GGA CCC CAG AAC AAG CAA CCC TTC ATG Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys Gln Pro Phe Met 265 270 275	931
GTG GCC TTC TTC AAG GCC ACG GAA GTC CAT CTC CGT AGT ATC CGG TCC Val Ala Phe Phe Lys Ala Thr Glu Val His Leu Arg Ser Ile Arg Ser 280 285 290	979
ACG GGG GGC AAG CAG CGC AGC CAG AAT CGC TCC AAG ACG CCA AAG AAC Thr Gly Gly Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro Lys Asn 295 300 305	1027
CAA GAG GCC CTG AGG ATG GCC AGT GTG GCA GAA AAC AGC AGC AGT GAC Gln Glu Ala Leu Arg Met Ala Ser Val Ala Glu Asn Ser Ser Ser Asp 310 315 320	1075

CAG AGG CAG GCC TGC AAG AAA CAT GAG CTG TAC GTC AGC TTC CGA GAC Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp 325 330 335 340	1123
CTT GGC TGG CAG GAC TGG ATC ATT GCA CCT GAA GGC TAT GCT GCC TAC Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Tyr 345 350 355	1171
TAC TGT GAG GGA GAG TGC GCC TTC CCT CTG AAC TCC TAC ATG AAC GCC Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn Ala 360 365 370	1219
ACC AAC CAC GCC ATC GTC CAG ACA CTG GTT CAC TTC ATC AAC CCA GAC Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn Pro Asp 375 380 385	1267
ACA GTA CCC AAG CCC TGC TGT GCG CCC ACC CAG CTC AAC GCC ATC TCT Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Glu Leu Asn Ala Ile Ser 390 395 400	1315
GTC CTC TAC TTC GAC GAC AGC TCT AAT GTC ATC CTG AAG AAG TAC AGA Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg 405 410 415 420	1363
AAC ATG GTG GTC CGG GCC TGT GGC TGC CAC TAGCTCTTCC TGAGACCCTG Asn Met Val Val Arg Ala Cys Gly Cys His 425 430	1413
ACCTTTGCGG GGCCACACCT TTCCAAATCT TCGATGTCTC ACCATCTAAG TCTCTCACTG	1473
CCCACCTTGG CGAGGAGAAC AGACCAACCT CTCCTGAGCC TTCCCTCACC TCCCAACCGG	1533
AAGCATGTAA GGGTTCCAGA AACCTGAGCG TGCAGCAGCT GATGAGCGCC CTTTCCTTCT	1593
GGCACGTGAC GGACAAGATC CTACCAGCTA CCACAGCAAA CGCCTAAGAG CAGGAAAAAT	1653
GTCTGCCAGG AAAGTGTC CA GTGTCCACAT GGCCCCTGGC GCTCTGAGTC TTTGAGGAGT	1713
AATCGCAAGC CTCGTTGAGC TGCAGCAGAA GGAAGGGCTT AGCCAGGGTG GCGCTGGCG	1773
TCTGTGTTGA AGGGAAACCA AGCAGAAGCC ACTGTAATGA TATGTCACAA TAAAACCCAT	1833
GAATGAAAAA AAAAAAAAAA AAAAAAAAAA AAAAGAATTC	1873

20) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (D) OTHER INFORMATION: /product= "mOP1-PP"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```

Met His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala
 1              5              10              15
Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser
      20              25              30
Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser
      35              40              45
Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu
      50              55              60
Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro
      65              70              75              80
Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Ser Gly
      85              90              95
Pro Asp Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr
      100              105              110
Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp
      115              120              125
Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys Glu
      130              135              140
Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser
      145              150              155              160
Lys Ile Pro Glu Gly Glu Arg Val Thr Ala Ala Glu Phe Arg Ile Tyr
      165              170              175
Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Gln Ile Thr
      180              185              190
Val Tyr Gln Val Leu Gln Glu His Ser Gly Arg Glu Ser Asp Leu Phe
      195              200              205

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Leu Leu Asp Ser Arg Thr Ile Trp Ala Ser Glu Glu Gly Trp Leu Val
 210 215 220
 Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg His
 225 230 235 240
 Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile
 245 250 255
 Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys
 260 265 270
 Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Leu Arg
 275 280 285
 Ser Ile Arg Ser Thr Gly Gly Lys Gln Arg Ser Gln Asn Arg Ser Lys
 290 295 300
 Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Ser Val Ala Glu Asn
 305 310 315 320
 Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val
 325 330 335
 Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly
 340 345 350
 Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser
 355 360 365
 Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe
 370 375 380
 Ile Asn Pro Asp Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu
 385 390 395 400
 Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu
 405 410 415
 Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
 420 425 430

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1723 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (F) TISSUE TYPE: HIPPOCAMPUS

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 490..1696
- (D) OTHER INFORMATION: /note= "hOP2 (cDNA)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

GGCGCCGGCA GAGCAGGAGT GGCTGGAGGA GCTGTGGTTG GAGCAGGAGG TGGCACGGCA      60
GGGCTGGAGG GCTCCCTATG AGTGGCGGAG ACGGCCCAGG AGGCGCTGGA GCAACAGCTC      120
CCACACCGCA CCAAGCGGTG GCTGCAGGAG CTCGCCCATC GCCCCTGCGC TGCTCGGACC      180
GCGGCCACAG CCGGACTGGC GGGTACGGCG GCGACAGAGG CATTGGCCGA GAGTCCCAGT      240
CCGCAGAGTA GCCCGGCCT CGAGGCGGTG GCGTCCCGGT CCTCTCCGTC CAGGAGCCAG      300
GACAGGTGTC GCGCGGCGGG GCTCCAGGGA CCGCGCCTGA GGCCGGCTGC CCGCCCGTCC      360
CGCCCCGCCC CGCCGCCCCG CGCCGCCGA GCCCAGCCTC CTTGCCGTCG GGGCGTCCCC      420
AGGCCCTGGG TCGGCCGCGG AGCCGATGCG CGCCCGCTGA GCGCCCCAGC TGAGCGCCCC      480
CGGCCTGCC ATG ACC GCG CTC CCC GGC CCG CTC TGG CTC CTG GGC CTG      528
      Met Thr Ala Leu Pro Gly Pro Leu Trp Leu Leu Gly Leu
          1             5             10

GCG CTA TGC GCG CTG GGC GGG GGC GGC CCC GGC CTG CGA CCC CCG CCC      576
Ala Leu Cys Ala Leu Gly Gly Gly Gly Pro Gly Leu Arg Pro Pro Pro
      15             20             25

GGC TGT CCC CAG CGA CGT CTG GGC GCG CGC GAG CGC CGG GAC GTG CAG      624
Gly Cys Pro Gln Arg Arg Leu Gly Ala Arg Glu Arg Arg Asp Val Gln
      30             35             40             45

CGC GAG ATC CTG GCG GTG CTC GGG CTG CCT GGG CGG CCC CGG CCC CGC      672
Arg Glu Ile Leu Ala Val Leu Gly Leu Pro Gly Arg Pro Arg Pro Arg
          50             55             60

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GCG CCA CCC GCC GCC TCC CGG CTG CCC GCG TCC GCG CCG CTC TTC ATG Ala Pro Pro Ala Ala Ser Arg Leu Pro Ala Ser Ala Pro Leu Phe Met 65 70 75	720
CTG GAC CTG TAC CAC GCC ATG GCC GGC GAC GAC GAC GAG GAC GGC GCG Leu Asp Leu Tyr His Ala Met Ala Gly Asp Asp Asp Glu Asp Gly Ala 80 85 90	768
CCC GCG GAG CGG CGC CTG GGC CGC GCC GAC CTG GTC ATG AGC TTC GTT Pro Ala Glu Arg Arg Leu Gly Arg Ala Asp Leu Val Met Ser Phe Val 95 100 105	816
AAC ATG GTG GAG CGA GAC CGT GCC CTG GGC CAC CAG GAG CCC CAT TGG Asn Met Val Glu Arg Asp Arg Ala Leu Gly His Gln Glu Pro His Trp 110 115 120 125	864
AAG GAG TTC CGC TTT GAC CTG ACC CAG ATC CCG GCT GGG GAG GCG GTC Lys Glu Phe Arg Phe Asp Leu Thr Gln Ile Pro Ala Gly Glu Ala Val 130 135 140	912
ACA GCT GCG GAG TTC CGG ATT TAC AAG GTG CCC AGC ATC CAC CTG CTC Thr Ala Ala Glu Phe Arg Ile Tyr Lys Val Pro Ser Ile His Leu Leu 145 150 155	960
AAC AGG ACC CTC CAC GTC AGC ATG TTC CAG GTG GTC CAG GAG CAG TCC Asn Arg Thr Leu His Val Ser Met Phe Gln Val Val Gln Glu Gln Ser 160 165 170	1008
AAC AGG GAG TCT GAC TTG TTC TTT TTG GAT CTT CAG ACG CTC CGA GCT Asn Arg Glu Ser Asp Leu Phe Phe Leu Asp Leu Gln Thr Leu Arg Ala 175 180 185	1056
GGA GAC GAG GGC TGG CTG GTG CTG GAT GTC ACA GCA GCC AGT GAC TGC Gly Asp Glu Gly Trp Leu Val Leu Asp Val Thr Ala Ala Ser Asp Cys 190 195 200 205	1104
TGG TTG CTG AAG CGT CAC AAG GAC CTG GGA CTC CGC CTC TAT GTG GAG Trp Leu Leu Lys Arg His Lys Asp Leu Gly Leu Arg Leu Tyr Val Glu 210 215 220	1152
ACT GAG GAC GGG CAC AGC GTG GAT CCT GGC CTG GCC GGC CTG CTG GGT Thr Glu Asp Gly His Ser Val Asp Pro Gly Leu Ala Gly Leu Leu Gly 225 230 235	1200
CAA CGG GCC CCA CGC TCC CAA CAG CCT TTC GTG GTC ACT TTC TTC AGG Gln Arg Ala Pro Arg Ser Gln Gln Pro Phe Val Val Thr Phe Phe Arg 240 245 250	1248
GCC AGT CCG AGT CCC ATC CGC ACC CCT CGG GCA GTG AGG CCA CTG AGG Ala Ser Pro Ser Pro Ile Arg Thr Pro Arg Ala Val Arg Pro Leu Arg 255 260 265	1296

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) OTHER INFORMATION: /product= "hOP2-PP"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```

Met Thr Ala Leu Pro Gly Pro Leu Trp Leu Leu Gly Leu Ala Leu Cys
 1             5             10             15
Ala Leu Gly Gly Gly Gly Pro Gly Leu Arg Pro Pro Pro Gly Cys Pro
          20             25             30
Gln Arg Arg Leu Gly Ala Arg Glu Arg Arg Asp Val Gln Arg Glu Ile
          35             40             45
Leu Ala Val Leu Gly Leu Pro Gly Arg Pro Arg Pro Arg Ala Pro Pro
          50             55             60
Ala Ala Ser Arg Leu Pro Ala Ser Ala Pro Leu Phe Met Leu Asp Leu
          65             70             75             80
Tyr His Ala Met Ala Gly Asp Asp Asp Glu Asp Gly Ala Pro Ala Glu
          85             90             95
Arg Arg Leu Gly Arg Ala Asp Leu Val Met Ser Phe Val Asn Met Val
          100            105            110
Glu Arg Asp Arg Ala Leu Gly His Gln Glu Pro His Trp Lys Glu Phe
          115            120            125
Arg Phe Asp Leu Thr Gln Ile Pro Ala Gly Glu Ala Val Thr Ala Ala
          130            135            140
Glu Phe Arg Ile Tyr Lys Val Pro Ser Ile His Leu Leu Asn Arg Thr
          145            150            155            160
Leu His Val Ser Met Phe Gln Val Val Gln Glu Gln Ser Asn Arg Glu
          165            170            175
Ser Asp Leu Phe Phe Leu Asp Leu Gln Thr Leu Arg Ala Gly Asp Glu
          180            185            190
Gly Trp Leu Val Leu Asp Val Thr Ala Ala Ser Asp Cys Trp Leu Leu
          195            200            205

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Lys Arg His Lys Asp Leu Gly Leu Arg Leu Tyr Val Glu Thr Glu Asp
 210 215 220
 Gly His Ser Val Asp Pro Gly Leu Ala Gly Leu Leu Gly Gln Arg Ala
 225 230 235 240
 Pro Arg Ser Gln Gln Pro Phe Val Val Thr Phe Phe Arg Ala Ser Pro
 245 250 255
 Ser Pro Ile Arg Thr Pro Arg Ala Val Arg Pro Leu Arg Arg Arg Gln
 260 265 270
 Pro Lys Lys Ser Asn Glu Leu Pro Gln Ala Asn Arg Leu Pro Gly Ile
 275 280 285
 Phe Asp Asp Val His Gly Ser His Gly Arg Gln Val Cys Arg Arg His
 290 295 300
 Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu Asp Trp Val Ile
 305 310 315 320
 Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr Cys Glu Gly Glu Cys Ser Phe
 325 330 335
 Pro Leu Asp Ser Cys Met Asn Ala Thr Asn His Ala Ile Leu Gln Ser
 340 345 350
 Leu Val His Leu Met Lys Pro Asn Ala Val Pro Lys Ala Cys Cys Ala
 355 360 365
 Pro Thr Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp Ser Ser Asn
 370 375 380
 Asn Val Ile Leu Arg Lys His Arg Asn Met Val Val Lys Ala Cys Gly
 385 390 395 400
 Cys His

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1926 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: MURIDAE
- (F) TISSUE TYPE: EMBRYO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 93..1289
- (D) OTHER INFORMATION: /note= "mOP2 cDNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```

GCCAGGCACA GGTGCGCCGT CTGGTCCTCC CCGTCTGGCG TCAGCCGAGC      50
CCGACCAGCT ACCAGTGGAT GCGCGCCGGC TGAAAGTCCG AG ATG GCT ATG CGT      104
                                   Met Ala Met Arg
                                   1
CCC GGG CCA CTC TGG CTA TTG GGC CTT GCT CTG TGC GCG CTG GGA GGC      152
Pro Gly Pro Leu Trp Leu Leu Gly Leu Ala Leu Cys Ala Leu Gly Gly
  5                      10                      15                      20
GGC CAC GGT CCG CGT CCC CCG CAC ACC TGT CCC CAG CGT CGC CTG GGA      200
Gly His Gly Pro Arg Pro Pro His Thr Cys Pro Gln Arg Arg Leu Gly
                      25                      30                      35
GCG CGC GAG CGC CGC GAC ATG CAG CGT GAA ATC CTG GCG GTG CTC GGG      248
Ala Arg Glu Arg Arg Asp Met Gln Arg Glu Ile Leu Ala Val Leu Gly
                      40                      45                      50
CTA CCG GGA CGG CCC CGA CCC CGT GCA CAA CCC GCG GCT GCC CGG CAG      296
Leu Pro Gly Arg Pro Arg Pro Arg Ala Gln Pro Ala Ala Ala Arg Gln
                      55                      60                      65
CCA GCG TCC GCG CCC CTC TTC ATG TTG GAC CTA TAC CAC GCC ATG ACC      344
Pro Ala Ser Ala Pro Leu Phe Met Leu Asp Leu Tyr His Ala Met Thr
  70                      75                      80
GAT GAC GAC GAC GGC GGG CCA CCA CAG GCT CAC TTA GGC CGT GCC GAC      392
Asp Asp Asp Asp Gly Gly Pro Pro Gln Ala His Leu Gly Arg Ala Asp
  85                      90                      95                      100

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CTG GTC ATG AGC TTC GTC AAC ATG GTG GAA CGC GAC CGT ACC CTG GGC	440
Leu Val Met Ser Phe Val Asn Met Val Glu Arg Asp Arg Thr Leu Gly	
105 110 115	
TAC CAG GAG CCA CAC TGG AAG GAA TTC CAC TTT GAC CTA ACC CAG ATC	488
Tyr Gln Glu Pro His Trp Lys Glu Phe His Phe Asp Leu Thr Gln Ile	
120 125 130	
CCT GCT GGG GAG GCT GTC ACA GCT GCT GAG TTC CGG ATC TAC AAA GAA	536
Pro Ala Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Glu	
135 140 145	
CCC AGC ACC CAC CCG CTC AAC ACA ACC CTC CAC ATC AGC ATG TTC GAA	584
Pro Ser Thr His Pro Leu Asn Thr Thr Leu His Ile Ser Met Phe Glu	
150 155 160	
GTG GTC CAA GAG CAC TCC AAC AGG GAG TCT GAC TTG TTC TTT TTG GAT	632
Val Val Gln Glu His Ser Asn Arg Glu Ser Asp Leu Phe Phe Leu Asp	
165 170 175 180	
CTT CAG ACG CTC CGA TCT GGG GAC GAG GGC TGG CTG GTG CTG GAC ATC	680
Leu Gln Thr Leu Arg Ser Gly Asp Glu Gly Trp Leu Val Leu Asp Ile	
185 190 195	
ACA GCA GCC AGT GAC CGA TGG CTG CTG AAC CAT CAC AAG GAC CTG GGA	728
Thr Ala Ala Ser Asp Arg Trp Leu Leu Asn His His Lys Asp Leu Gly	
200 205 210	
CTC CGC CTC TAT GTG GAA ACC GCG GAT GGG CAC AGC ATG GAT CCT GGC	776
Leu Arg Leu Tyr Val Glu Thr Ala Asp Gly His Ser Met Asp Pro Gly	
215 220 225	
CTG GCT GGT CTG CTT GGA CGA CAA GCA CCA CGC TCC AGA CAG CCT TTC	824
Leu Ala Gly Leu Leu Gly Arg Gln Ala Pro Arg Ser Arg Gln Pro Phe	
230 235 240	
ATG GTA ACC TTC TTC AGG GCC AGC CAG AGT CCT GTG CGG GCC CCT CGG	872
Met Val Thr Phe Phe Arg Ala Ser Gln Ser Pro Val Arg Ala Pro Arg	
245 250 255 260	
GCA GCG AGA CCA CTG AAG AGG AGG CAG CCA AAG AAA ACG AAC GAG CTT	920
Ala Ala Arg Pro Leu Lys Arg Arg Gln Pro Lys Lys Thr Asn Glu Leu	
265 270 275	
CCG CAC CCC AAC AAA CTC CCA GGG ATC TTT GAT GAT GGC CAC GGT TCC	968
Pro His Pro Asn Lys Leu Pro Gly Ile Phe Asp Asp Gly His Gly Ser	
280 285 290	
CGC GGC AGA GAG GTT TGC CGC AGG CAT GAG CTC TAC GTC AGC TTC CGT	1016
Arg Gly Arg Glu Val Cys Arg Arg His Glu Leu Tyr Val Ser Phe Arg	
295 300 305	

GAC CTT GGC TGG CTG GAC TGG GTC ATC GCC CCC CAG GGC TAC TCT GCC Asp Leu Gly Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala 310 315 320	1064
TAT TAC TGT GAG GGG GAG TGT GCT TTC CCA CTG GAC TCC TGT ATG AAC Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asp Ser Cys Met Asn 325 330 335 340	1112
GCC ACC AAC CAT GCC ATC TTG CAG TCT CTG GTG CAC CTG ATG AAG CCA Ala Thr Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met Lys Pro 345 350 355	1160
GAT GTT GTC CCC AAG GCA TGC TGT GCA CCC ACC AAA CTG AGT GCC ACC Asp Val Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr 360 365 370	1208
TCT GTG CTG TAC TAT GAC AGC AGC AAC AAT GTC ATC CTG CGT AAA CAC Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His 375 380 385	1256
CGT AAC ATG GTG GTC AAG GCC TGT GGC TGC CAC TGAGGCCCG CCCAGCATCC Arg Asn Met Val Val Lys Ala Cys Gly Cys His 390 395	1309
TGCTTCTACT ACCTTACCAT CTGGCCGGGC CCCTCTCCAG AGGCAGAAAC CCTTCTATGT	1369
TATCATAGCT CAGACAGGGG CAATGGGAGG CCCTTCACTT CCCCTGGCCA CTTCTGCTA	1429
AAATTCTGGT CTTTCCCAGT TCCTCTGTCC TTCATGGGGT TTCGGGGCTA TCACCCCGCC	1489
CTCTCCATCC TCCTACCCCA AGCATAGACT GAATGCACAC AGCATCCCAG AGCTATGCTA	1549
ACTGAGAGGT CTGGGGTCAG CACTGAAGGC CCACATGAGG AAGACTGATC CTTGGCCATC	1609
CTCAGCCCAC AATGGCAAAT TCTGGATGGT CTAAGAAGGC CGTGGAATTC TAAACTAGAT	1669
GATCTGGGCT CTCTGCACCA TTCATTGTGG CAGTTGGGAC ATTTTtagGT ATAACAGACA	1729
CATACACTTA GATCAATGCA TCGCTGTACT CCTTGAAATC AGAGCTAGCT TGTTAGAAAA	1789
AGAATCAGAG CCAGGTATAG CGGTGCATGT CATTAAATCCC AGCGCTAAAG AGACAGAGAC	1849
AGGAGAATCT CTGTGAGTTC AAGGCCACAT AGAAAGAGCC TGTCTCGGGA GCAGGAAAAA	1909
AAAAAAAAAC GGAATTC	1926

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 399 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(D) OTHER INFORMATION: /product= "mOP2-PP"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```

Met Ala Met Arg Pro Gly Pro Leu Trp Leu Leu Gly Leu Ala Leu Cys
 1           5           10           15
Ala Leu Gly Gly Gly His Gly Pro Arg Pro Pro His Thr Cys Pro Gln
          20           25           30
Arg Arg Leu Gly Ala Arg Glu Arg Arg Asp Met Gln Arg Glu Ile Leu Ala
          35           40           45
Val Leu Gly Leu Pro Gly Arg Pro Arg Pro Arg Ala Gln Pro Ala Ala
 50           55           60           65
Ala Arg Gln Pro Ala Ser Ala Pro Leu Phe Met Leu Asp Leu Tyr His Ala
          70           75           80
Met Thr Asp Asp Asp Asp Gly Gly Pro Pro Gln Ala His Leu Gly Arg
          85           90           95
Ala Asp Leu Val Met Ser Phe Val Asn Met Val Glu Arg Asp Arg Thr
 100           105           110
Leu Gly Tyr Gln Glu Pro His Trp Lys Glu Phe His Phe Asp Leu Thr
 115           120           125           130
Gln Ile Pro Ala Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr
          135           140           145
Lys Glu Pro Ser Thr His Pro Leu Asn Thr Thr Leu His Ile Ser Met
          150           155           160
Phe Glu Val Val Gln Glu His Ser Asn Arg Glu Ser Asp Leu Phe Phe
          165           170           175
Leu Asp Leu Gln Thr Leu Arg Ser Gly Asp Glu Gly Trp Leu Val Leu
          180           185           190
Asp Ile Thr Ala Ala Ser Asp Arg Trp Leu Leu Asn His His Lys Asp
 195           200           205           210

```

Leu Gly Leu Arg Leu Tyr Val Glu Thr Ala Asp Gly His Ser Met Asp
 215 220 225
 Pro Gly Leu Ala Gly Leu Leu Gly Arg Gln Ala Pro Arg Ser Arg Gln
 230 235 240
 Pro Phe Met Val Thr Phe Phe Arg Ala Ser Gln Ser Pro Val Arg Ala
 245 250 255
 Pro Arg Ala Ala Arg Pro Leu Lys Arg Arg Gln Pro Lys Lys Thr Asn
 260 265 270
 Glu Leu Pro His Pro Asn Lys Leu Pro Gly Ile Phe Asp Asp Gly His
 275 280 285 290
 Gly Ser Arg Gly Arg Glu Val Cys Arg Arg His Glu Leu Tyr Val Ser
 295 300 305
 Phe Arg Asp Leu Gly Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr
 310 315 320
 Ser Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asp Ser Cys
 325 330 335
 Met Asn Ala Thr Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met
 340 345 350
 Lys Pro Asp Val Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser
 355 360 365 370
 Ala Thr Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg
 375 380 385
 Lys His Arg Asn Met Val Val Lys Ala Cys Gly Cys His
 390 395

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1368 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1368
- (D) OTHER INFORMATION: /STANDARD NAME="60A"

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: WHARTON, KRISTI A.; THOMSEN, GERALD H.; GELBERT, WILLIAM M.
- (B) TITLE: DROSOPHILA 60A GENE...
- (C) JOURNAL: PROC. NAT'L ACAD. SCI. USA
- (D) VOLUME: 88
- (E) RELEVANT RESIDUES IN SEQ ID NO:3: FROM 1 TO 1368
- (F) PAGES: 9214-9218
- (G) DATE: OCT - 1991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATG TCG GGA CTG CGA AAC ACC TCG GAG GCC GTT GCA GTG CTC GCC TCC	48
Met Ser Gly Leu Arg Asn Thr Ser Glu Ala Val Ala Val Leu Ala Ser	
1 5 10 15	
CTG GGA CTC GGA ATG GTT CTG CTC ATG TTC GTG GCG ACC ACG CCG CCG	96
Leu Gly Leu Gly Met Val Leu Leu Met Phe Val Ala Thr Thr Pro Pro	
20 25 30	
GCC GTT GAG GCC ACC CAG TCG GGG ATT TAC ATA GAC AAC GGC AAG GAC	144
Ala Val Glu Ala Thr Gln Ser Gly Ile Tyr Ile Asp Asn Gly Lys Asp	
35 40 45	
CAG ACG ATC ATG CAC AGA GTG CTG AGC GAG GAC GAC AAG CTG GAC GTC	192
Gln Thr Ile Met His Arg Val Leu Ser Glu Asp Asp Lys Leu Asp Val	
50 55 60	
TCG TAC GAG ATC CTC GAG TTC CTG GGC ATC GCC GAA CGG CCG ACG CAC	240
Ser Tyr Glu Ile Leu Glu Phe Leu Gly Ile Ala Glu Arg Pro Thr His	
65 70 75 80	
CTG AGC AGC CAC CAG TTG TCG CTG AGG AAG TCG GCT CCC AAG TTC CTG	288
Leu Ser Ser His Gln Leu Ser Leu Arg Lys Ser Ala Pro Lys Phe Leu	
85 90 95	

CTG GAC GTC TAC CAC CGC ATC ACG GCG GAG GAG GGT CTC AGC GAT CAG Leu Asp Val Tyr His Arg Ile Thr Ala Glu Glu Gly Leu Ser Asp Gln 100 105 110	336
GAT GAG GAC GAC GAC TAC GAA CGC GGC CAT CGG TCC AGG AGG AGC GCC Asp Glu Asp Asp Asp Tyr Glu Arg Gly His Arg Ser Arg Arg Ser Ala 115 120 125	384
GAC CTC GAG GAG GAT GAG GGC GAG CAG CAG AAG AAC TTC ATC ACC GAC Asp Leu Glu Glu Asp Glu Gly Glu Gln Gln Lys Asn Phe Ile Thr Asp 130 135 140	432
CTG GAC AAG CGG GCC ATC GAC GAG AGC GAC ATC ATC ATG ACC TTC CTG Leu Asp Lys Arg Ala Ile Asp Glu Ser Asp Ile Ile Met Thr Phe Leu 145 150 155 160	480
AAC AAG CGC CAC CAC AAT GTG GAC GAA CTG CGT CAC GAG CAC GGC CGT Asn Lys Arg His His Asn Val Asp Glu Leu Arg His Glu His Gly Arg 165 170 175	528
CGC CTG TGG TTC GAC GTC TCC AAC GTG CCC AAC GAC AAC TAC CTG GTG Arg Leu Trp Phe Asp Val Ser Asn Val Pro Asn Asp Asn Tyr Leu Val 180 185 190	576
ATG GCC GAG CTG CGC ATC TAT CAG AAC GCC AAC GAG GGC AAG TGG CTG Met Ala Glu Leu Arg Ile Tyr Gln Asn Ala Asn Glu Gly Lys Trp Leu 195 200 205	624
ACC GCC AAC AGG GAG TTC ACC ATC ACG GTA TAC GCC ATT GGC ACC GGC Thr Ala Asn Arg Glu Phe Thr Ile Thr Val Tyr Ala Ile Gly Thr Gly 210 215 220	672
ACG CTG GGC CAG CAC ACC ATG GAG CCG CTG TCC TCG GTG AAC ACC ACC Thr Leu Gly Gln His Thr Met Glu Pro Leu Ser Ser Val Asn Thr Thr 225 230 235 240	720
GGG GAC TAC GTG GGC TGG TTG GAG CTC AAC GTG ACC GAG GGC CTG CAC Gly Asp Tyr Val Gly Trp Leu Glu Leu Asn Val Thr Glu Gly Leu His 245 250 255	768
GAG TGG CTG GTC AAG TCG AAG GAC AAT CAT GGC ATC TAC ATT GGA GCA Glu Trp Leu Val Lys Ser Lys Asp Asn His Gly Ile Tyr Ile Gly Ala 260 265 270	816
CAC GCT GTC AAC CGA CCC GAC CGC GAG GTG AAG CTG GAC GAC ATT GGA His Ala Val Asn Arg Pro Asp Arg Glu Val Lys Leu Asp Asp Ile Gly 275 280 285	864
CTG ATC CAC CGC AAG GTG GAC GAC GAG TTC CAG CCC TTC ATG ATC GGC Leu Ile His Arg Lys Val Asp Asp Glu Phe Gln Pro Phe Met Ile Gly 290 295 300	912

[illegible]

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 455 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```

Met Ser Gly Leu Arg Asn Thr Ser Glu Ala Val Ala Val Leu Ala Ser
 1           5           10           15
Leu Gly Leu Gly Met Val Leu Leu Met Phe Val Ala Thr Thr Pro Pro
          20           25           30
Ala Val Glu Ala Thr Gln Ser Gly Ile Tyr Ile Asp Asn Gly Lys Asp
          35           40           45
Gln Thr Ile Met His Arg Val Leu Ser Glu Asp Asp Lys Leu Asp Val
          50           55           60
Ser Tyr Glu Ile Leu Glu Phe Leu Gly Ile Ala Glu Arg Pro Thr His
          65           70           75           80
Leu Ser Ser His Gln Leu Ser Leu Arg Lys Ser Ala Pro Lys Phe Leu
          85           90           95
Leu Asp Val Tyr His Arg Ile Thr Ala Glu Glu Gly Leu Ser Asp Gln
          100          105          110
Asp Glu Asp Asp Asp Tyr Glu Arg Gly His Arg Ser Arg Arg Ser Ala
          115          120          125
Asp Leu Glu Glu Asp Glu Gly Glu Gln Gln Lys Asn Phe Ile Thr Asp
          130          135          140
Leu Asp Lys Arg Ala Ile Asp Glu Ser Asp Ile Ile Met Thr Phe Leu
          145          150          155          160
Asn Lys Arg His His Asn Val Asp Glu Leu Arg His Glu His Gly Arg
          165          170          175
Arg Leu Trp Phe Asp Val Ser Asn Val Pro Asn Asp Asn Tyr Leu Val
          180          185          190
Met Ala Glu Leu Arg Ile Tyr Gln Asn Ala Asn Glu Gly Lys Trp Leu
          195          200          205
Thr Ala Asn Arg Glu Phe Thr Ile Thr Val Tyr Ala Ile Gly Thr Gly
          210          215          220

```

Thr Leu Gly Gln His Thr Met Glu Pro Leu Ser Ser Val Asn Thr Thr
 225 230 235 240
 Gly Asp Tyr Val Gly Trp Leu Glu Leu Asn Val Thr Glu Gly Leu His
 245 250 255
 Glu Trp Leu Val Lys Ser Lys Asp Asn His Gly Ile Tyr Ile Gly Ala
 260 265 270
 His Ala Val Asn Arg Pro Asp Arg Glu Val Lys Leu Asp Asp Ile Gly
 275 280 285
 Leu Ile His Arg Lys Val Asp Asp Glu Phe Gln Pro Phe Met Ile Gly
 290 295 300
 Phe Phe Arg Gly Pro Glu Leu Ile Lys Ala Thr Ala His Ser Ser His
 305 310 315 320
 His Arg Ser Lys Arg Ser Ala Ser His Pro Arg Lys Arg Lys Lys Ser
 325 330 335
 Val Ser Pro Asn Asn Val Pro Leu Leu Glu Pro Met Glu Ser Thr Arg
 340 345 350
 Ser Cys Gln Met Gln Thr Leu Tyr Ile Asp Phe Lys Asp Leu Gly Trp
 355 360 365
 His Asp Trp Ile Ile Ala Pro Glu Gly Tyr Gly Ala Phe Tyr Cys Ser
 370 375 380
 Gly Glu Cys Asn Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His
 385 390 395 400
 Ala Ile Val Gln Thr Leu Val His Leu Leu Glu Pro Lys Lys Val Pro
 405 410 415
 Lys Pro Cys Cys Ala Pro Thr Arg Leu Gly Ala Leu Pro Val Leu Tyr
 420 425 430
 His Leu Asn Asp Glu Asn Val Asn Leu Lys Lys Tyr Arg Asn Met Ile
 435 440 445
 Val Lys Ser Cys Gly Cys His
 450 455

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: /note="BMP3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: /note="BMP3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```

Cys Ala Arg Arg Tyr Leu Lys Val Asp Phe Ala Asp Ile Gly Trp Ser
1           5           10           15
Glu Trp Ile Ile Ser Pro Lys Ser Phe Asp Ala Tyr Try Cys Ser Gly
20           25           30
Ala Cys Gln Phe Pro Met Pro Lys Ser Leu Lys Pro Ser Asn His Ala
35           40           45
Thr Ile Gln Ser Ile Val Ala Arg Ala Val Gly Val Val Pro Gly Ile
50           55           60
Pro Glu Pro Cys Cys Val Pro Glu Lys Met Ser Ser Leu Ser Ile Leu
65           70           75           80
Phe Phe Asp Glu Asn Lys Asn Val Val Leu Lys Val Tyr Pro Asn Met
85           90           95
Thr Val Glu Ser Cys Ala Cys Arg
100

```

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: HOMO SAPIENS

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: /note= "BMP5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```

Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Gln
1           5           10           15
Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Phe Tyr Cys Asp Gly
20           25           30
Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His Ala
35           40           45
Ile Val Gln Thr Leu Val His Leu Met Phe Pro Asp His Val Pro Lys
50           55           60
Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe
65           70           75           80
Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val
85           90           95
Arg Ser Cys Gly Cys His
100

```

(2) INFORMATION FOR SEQ ID NO:28:

- ```
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: HOMO SAPIENS

(ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..102
 (D) OTHER INFORMATION: /note= "BMP6"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:
```

[illegible]

## (2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 102 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (ix) FEATURE:  
 (A) NAME/KEY: Protein  
 (B) LOCATION: 1..102  
 (D) OTHER INFORMATION: /label= OPX  
 /note= "WHEREIN XAA AT EACH POS'N IS INDEPENDENTLY  
 SELECTED FROM THE RESIDUES OCCURRING AT THE  
 CORRESPONDING POS'N IN THE C-TERMINAL SEQUENCE OF MOUSE  
 OR HUMAN OP1 OR OP2 (SEE SEQ. ID NOS. 5,6,7 and 8 or  
 16,18,20 and 22.)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```

Cys Xaa Xaa His Glu Leu Tyr Val Xaa Phe Xaa Asp Leu Gly Trp Xaa
1 5 10 15
Asp Trp Xaa Ile Ala Pro Xaa Gly Tyr Xaa Ala Tyr Tyr Cys Glu Gly
20 25 30
Glu Cys Xaa Phe Pro Leu Xaa Ser Xaa Met Asn Ala Thr Asn His Ala
35 40 45
Ile Xaa Gln Xaa Leu Val His Xaa Xaa Xaa Pro Xaa Xaa Val Pro Lys
50 55 60
Xaa Cys Cys Ala Pro Thr Xaa Leu Xaa Ala Xaa Ser Val Leu Tyr Xaa
65 70 75 80
Asp Xaa Ser Xaa Asn Val Xaa Leu Xaa Lys Xaa Arg Asn Met Val Val
85 90 95
Xaa Ala Cys Gly Cys His
100

```

## (2) INFORMATION FOR SEQ ID NO:30:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acids

(C) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (ix) FEATURE:

(A) NAME: Generic Sequence 5

(D) OTHER INFORMATION: wherein each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification.

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```

Leu Xaa Xaa Xaa Phe
 1 5
Xaa Xaa Xaa Gly Trp Xaa Xaa Trp Xaa
 10
Xaa Xaa Pro Xaa Xaa Xaa Xaa Ala
 15 20
Xaa Tyr Cys Xaa Gly Xaa Cys Xaa
 25 30
Xaa Pro Xaa Xaa Xaa Xaa Xaa
 35
Xaa Xaa Xaa Asn His Ala Xaa Xaa
 40 45
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 50
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
 55 60
Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa
 65
Xaa Xaa Xaa Leu Xaa Xaa Xaa
 70 75
Xaa Xaa Xaa Xaa Val Xaa Leu Xaa
 80
Xaa Xaa Xaa Xaa Met Xaa Val Xaa
 85 90
Xaa Cys Xaa Cys Xaa
 95

```

## (2) INFORMATION FOR SEQ ID NO:31:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acids

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (ix) FEATURE:

(A) NAME: Generic Sequence 6

(D) OTHER INFORMATION: wherein each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification.

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Cys Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Phe

1 5 10

Xaa Xaa Xaa Gly Trp Xaa Xaa Trp Xaa

15

Xaa Xaa Pro Xaa Xaa Xaa Xaa Ala

20 25

Xaa Tyr Cys Xaa Gly Xaa Cys Xaa

30 35

Xaa Pro Xaa Xaa Xaa Xaa Xaa

40

Xaa Xaa Xaa Asn His Ala Xaa Xaa

45 50

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

55

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys

60 65

Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa

70

Xaa Xaa Xaa Leu Xaa Xaa Xaa

75 80

Xaa Xaa Xaa Xaa Val Xaa Leu Xaa

85

Xaa Xaa Xaa Xaa Met Xaa Val Xaa

90 95

Xaa Cys Xaa Cys Xaa

100

## (2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1238 base pairs, 372 amino acids
  - (B) TYPE: nucleic acid, amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) ORIGINAL SOURCE:
  - (A) ORGANISM: human
  - (F) TISSUE TYPE: BRAIN
- (iv) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION:
  - (D) OTHER INFORMATION:
    - /product= "GDF-1"
    - /note= "GDF-1 CDNA"
- (x) PUBLICATION INFORMATION:
  - (A) AUTHORS: Lee, Se-Jin
  - (B) TITLE: Expression of Growth/Differentiation Factor 1
  - (C) JOURNAL: Proc. Nat'l Acad. Sci.
  - (D) VOLUME: 88
  - (E) RELEVANT RESIDUES: 1-1238
  - (F) PAGES: 4250-4254
  - (G) DATE: May-1991
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```

GGGGACACCG GCGCCGCCCT CAGCCCACTG GTCCCGGGCC GCCGCGGACC CTGCGCACTC 60
TCTGGTCATC GCCTGGGAGG AAG ATG CCA CCG CCG CAG CAA GGT CCC TGC GGC 113
 Met Pro Pro Pro Gln Gln Gly Pro Cys Gly
 1 5 10

CAC CAC CTC CTC CTC CTC CTG GCC CTG CTG CTG CCC TCG CTG CCC 158
His His Leu Leu Leu Leu Leu Ala Leu Leu Leu Pro Ser Leu Pro
 15 20 25

CTG ACC CGC GCC CCC GTG CCC CCA GGC CCA GCC GCC GCC CTG CTC 203
Leu Thr Arg Ala Pro Val Pro Pro Gly Pro Ala Ala Ala Leu Leu
 30 35 40

CAG GCT CTA GGA CTG CGC GAT GAG CCC CAG GGT GCC CCC AGG CTC 248
Gln Ala Leu Gly Leu Arg Asp Glu Pro Gln Gly Ala Pro Arg Leu
 45 50 55

```

|                                                             |     |
|-------------------------------------------------------------|-----|
| CGG CCG GTT CCC CCG GTC ATG TGG CGC CTG TTT CGA CGC CGG GAC | 293 |
| Arg Pro Val Pro Pro Val Met Trp Arg Leu Phe Arg Arg Arg Asp |     |
| 60 65 70                                                    |     |
| CCC CAG GAG ACC AGG TCT GGC TCG CGG CGG ACG TCC CCA GGG GTC | 338 |
| Pro Gln Glu Thr Arg Ser Gly Ser Arg Arg Thr Ser Pro Gly Val |     |
| 75 80 85                                                    |     |
| ACC CTG CAA CCG TGC CAC GTG GAG GAG CTG GGG GTC GCC GGA AAC | 383 |
| Thr Leu Gln Pro Cys His Val Glu Glu Leu Gly Val Ala Gly Asn |     |
| 90 95 100                                                   |     |
| ATC GTG CGC CAC ATC CCG GAC CGC GGT GCG CCC ACC CGG GCC TCG | 428 |
| Ile Val Arg His Ile Pro Asp Arg Gly Ala Pro Thr Arg Ala Ser |     |
| 105 110 115                                                 |     |
| GAG CCT GTC TCG GCC GCG GGG CAT TGC CCT GAG TGG ACA GTC GTC | 473 |
| Glu Pro Val Ser Ala Ala Gly His Cys Pro Glu Trp Thr Val Val |     |
| 120 125 130                                                 |     |
| TTC GAC CTG TCG GCT GTG GAA CCC GCT GAG CGC CCG AGC CGG GCC | 518 |
| Phe Asp Leu Ser Ala Val Glu Pro Ala Glu Arg Pro Ser Arg Ala |     |
| 135 140 145                                                 |     |
| CGC CTG GAG CTG CGT TTC GCG GCG GCG GCG GCG GCA GCC CCG GAG | 563 |
| Arg Leu Glu Leu Arg Phe Ala Ala Ala Ala Ala Ala Ala Pro Glu |     |
| 150 155 160                                                 |     |
| GGC GGC TGG GAG CTG AGC GTG GCG CAA GCG GGC CAG GGC GCG GGC | 608 |
| Gly Gly Trp Glu Leu Ser Val Ala Gln Ala Gly Gln Gly Ala Gly |     |
| 165 170 175                                                 |     |
| GCG GAC CCC GGG CCG GTG CTG CTC CGC CAG TTG GTG CCC GCC CTG | 653 |
| Ala Asp Pro Gly Pro Val Leu Leu Arg Gln Leu Val Pro Ala Leu |     |
| 180 185 190                                                 |     |
| GGG CCG CCA GTG CGC GCG GAG CTG CTG GGC GCC GCT TGG GCT CGC | 698 |
| Gly Pro Pro Val Arg Ala Glu Leu Leu Gly Ala Ala Trp Ala Arg |     |
| 195 200 205                                                 |     |
| AAC GCC TCA TGG CCG CGC AGC CTC CGC CTG GCG CTG GCG CTA CGC | 743 |
| Asn Ala Ser Trp Pro Arg Ser Leu Arg Leu Ala Leu Ala Leu Arg |     |
| 210 215 220                                                 |     |
| CCC CGG GCC CCT GCC GCC TGC GCG CGC CTG GCC GAG GCC TCG CTG | 788 |
| Pro Arg Ala Pro Ala Ala Cys Ala Arg Leu Ala Glu Ala Ser Leu |     |
| 225 230 235                                                 |     |
| CTG CTG GTG ACC CTC GAC CCG CGC CTG TGC CAC CCC CTG GCC CGG | 833 |
| Leu Leu Val Thr Leu Asp Pro Arg Leu Cys His Pro Leu Ala Arg |     |
| 240 245 250                                                 |     |

|                                                              |      |
|--------------------------------------------------------------|------|
| CCG CGG CGC GAC GCC GAA CCC GTG TTG GGC GGC GGC CCC GGG GGC  | 878  |
| Pro Arg Arg Asp Ala Glu Pro Val Leu Gly Gly Gly Pro Gly Gly  |      |
| 255 260 265                                                  |      |
| GCT TGT CGC GCG CGG CGG CTG TAC GTG AGC TTC CGC CAG GTG GGC  | 923  |
| Ala Cys Arg Ala Arg Arg Leu Tyr Val Ser Phe Arg Glu Val Gly  |      |
| 270 275 280                                                  |      |
| TGG CAC CGC TGG GTC ATC GCG CCG CGC CCC TTC CTG GCC AAC TAC  | 968  |
| Trp His Arg Trp Val Ile Arg Pro Arg Gly Phe Leu Ala Asn Tyr  |      |
| 285 290 295                                                  |      |
| TGC CAG GGT CAG TGC GCG CTG CCC GTC GCG CTG TCG GGG TCC GGC  | 1013 |
| Cys Gln Gly Gln Cys Ala Leu Pro Val Ala Leu Ser Gly Ser Gly  |      |
| 300 305 310                                                  |      |
| GGG CCG CCG GCG CTC AAC CAC GCT GTG CTG CGC GCG CTC ATG CAC  | 1058 |
| Gly Pro Pro Ala Leu Asn His Ala Val Leu Arg Ala Leu Met His  |      |
| 315 320 325                                                  |      |
| GCG GCC GCC CCG GGA GCC GCC GAC CTG CCC TGC TGC GTG CCC GCG  | 1103 |
| Ala Ala Ala Pro Gly Ala Ala Asp Leu Pro Cys Cys Val Pro Ala  |      |
| 330 335 340                                                  |      |
| CGC CTG TCG CCC ATC TCC GTG CTC TTC TTT GAC AAC AGC GAC AAC  | 1148 |
| Arg Leu Ser Pro Ile Ser Val Leu Phe Phe Asp Asn Ser Asp Asn  |      |
| 345 350 355                                                  |      |
| GTG GTG CTG CGG CAG TAT GAG GAC ATG GTG GTG GAC GAG TGC GGC  | 1193 |
| Val Val Leu Arg Gln Tyr Glu Asp Met Val Val Asp Glu Cys Gly  |      |
| 360 365 370                                                  |      |
| TGC CGC TAACCCGGGG CGGGCAGGGA CCCGGGCCCA ACAATAAATG CCGCGTGG | 1238 |
| Cys Arg                                                      |      |
| 372                                                          |      |

(34) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 372 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) **HYPOTHETICAL: NO**

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human  
(F) TISSUE TYPE: BRAIN

(ix) **FEATURE:**

- ```

(A) NAME/KEY: CDS
(B) LOCATION:
(D) OTHER INFORMATION: /function=
                        /product= "GDF-1"

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

						Met 1	Pro	Pro	Pro	Gln 5	Gln	Gly	Pro	Cys	Gly 10
His	His	Leu	Leu	Leu 15	Leu	Leu	Ala	Leu	Leu 20	Leu	Pro	Ser	Leu	Pro 25	
Leu	Thr	Arg	Ala	Pro 30	Val	Pro	Pro	Gly	Pro 35	Ala	Ala	Ala	Leu	Leu 40	
Gln	Ala	Leu	Gly	Leu 45	Arg	Asp	Glu	Pro	Gln 50	Gly	Ala	Pro	Arg	Leu 55	
Arg	Pro	Val	Pro	Pro 60	Val	Met	Trp	Arg	Leu 65	Phe	Arg	Arg	Arg	Asp 70	
Pro	Gln	Glu	Thr	Arg 75	Ser	Gly	Ser	Arg	Arg 80	Thr	Ser	Pro	Gly	Val 85	
Thr	Leu	Gln	Pro	Cyc 90	His	Val	Glu	Glu	Leu 95	Gly	Val	Ala	Gly	Asn 100	
Ile	Val	Arg	His	Ile 105	Pro	Asp	Arg	Gly	Ala 110	Pro	Thr	Arg	Ala	Ser 115	

Glu	Pro	Val	Ser	Ala	Ala	Gly	His	Cys	Pro	Glu	Trp	Thr	Val	Val	120	125	130
Phe	Asp	Leu	Ser	Ala	Val	Glu	Pro	Ala	Glu	Arg	Pro	Ser	Arg	Ala	135	140	145
Arg	Leu	Glu	Leu	Arg	Phe	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Pro	Glu	150	155	160
Gly	Gly	Trp	Glu	Leu	Ser	Val	Ala	Gln	Ala	Gly	Gln	Gly	Ala	Gly	165	170	175
Ala	Asp	Pro	Gly	Pro	Val	Leu	Leu	Arg	Gln	Leu	Val	Pro	Ala	Leu	180	185	190
Gly	Pro	Pro	Val	Arg	Ala	Glu	Leu	Leu	Gly	Ala	Ala	Trp	Ala	Arg	195	200	205
Asn	Ala	Ser	Trp	Pro	Arg	Ser	Leu	Arg	Leu	Ala	Leu	Ala	Leu	Arg	210	215	220
Pro	Arg	Ala	Pro	Ala	Ala	Cys	Ala	Arg	Leu	Ala	Glu	Ala	Ser	Leu	225	230	235
Leu	Leu	Val	Thr	Leu	Asp	Pro	Arg	Leu	Cys	His	Pro	Leu	Ala	Arg	240	245	250
Pro	Arg	Arg	Asp	Ala	Glu	Pro	Val	Leu	Gly	Gly	Gly	Pro	Gly	Gly	255	260	265
Ala	Cys	Arg	Ala	Arg	Arg	Leu	Tyr	Val	Ser	Phe	Arg	Glu	Val	Gly	270	275	280
Trp	His	Arg	Trp	Val	Ile	Arg	Pro	Arg	Gly	Phe	Leu	Ala	Asn	Tyr	285	290	295
Cys	Gln	Gly	Gln	Cys	Ala	Leu	Pro	Val	Ala	Leu	Ser	Gly	Ser	Gly	300	305	310
Gly	Pro	Pro	Ala	Leu	Asn	His	Ala	Val	Leu	Arg	Ala	Leu	Met	His	315	320	325
Ala	Ala	Ala	Pro	Gly	Ala	Ala	Asp	Leu	Pro	Cys	Cys	Val	Pro	Ala	330	335	340
Arg	Leu	Ser	Pro	Ile	Ser	Val	Leu	Phe	Phe	Asp	Asn	Ser	Asp	Asn	345	350	355
Val	Val	Leu	Arg	Gln	Tyr	Glu	Asp	Met	Val	Val	Asp	Glu	Cys	Gly	360	365	370
Cys	Arg														372		

What is claimed is:

1. A method of screening candidate compounds for the ability to modulate the effective concentration of a morphogen in an organism, said method comprising
incubating a candidate compound with cells from a test tissue type known to produce a morphogen for a time sufficient to allow said compound to affect the production of said morphogen, and
assaying said cells for a parameter indicative of a change in the level of production of said morphogen.
2. The method of claim 1 wherein said morphogen is OP-1.
3. The method of claim 2 wherein said test tissue type is a human renal-derived tissue.
4. The method of claim 3 wherein said renal-derived tissue is a kidney or bladder-derived tissue.
5. The method of claim 2 wherein said test tissue type is adrenal-derived tissue.
6. The method of claim 1 wherein said morphogen is GDF-1.
7. The method of claim 6 wherein said test tissue type is derived from human nerve tissue.

8. The method of claim 7 wherein said nerve tissue is brain-derived tissue.

9. The method of claim 1 wherein said morphogen is DPP.

10. The method of claim 9 wherein said test tissue type is derived from one of the following drosophila tissues: dorsal ectoderm, epithelial imaginal disc visceral mesoderm, or gut endoderm.

11. The method of claim 1 wherein said morphogen is Vgr-1.

12. The method of claim 11 wherein said test tissue type is mouse lung tissue.

13. The method of claim 1 wherein said morphogen is Vgl.

14. The method of claim 13 wherein said test tissue type is xenopus fetal endoderm tissue.

15. A method of assessing a tissue of an organism for its level of production of a morphogen and for screening candidate compounds for the ability to modulate the effective concentration of said morphogen produced by cells of said tissue, said method comprising

selecting a test tissue type producing a high level of morphogen relative to the level of morphogen produced by other tissue types;

incubating a candidate compound with cultured cells of said selected tissue type for a time sufficient to allow said compound to affect the production of said morphogen; and

assaying said selected tissue cells for a parameter indicative of a change in the level of production of said morphogen.

16. The method of claim 1 or 15 wherein said parameter indicative of the level of said morphogen is determined using an antibody specific for said morphogen.

17. The method of claim 1 or 15 wherein said parameter indicative of the level of said morphogen is determined by measuring cellular proliferation in cells which are sensitive to the concentration of secreted OP-1.

18. The method of claim 1 or 15 wherein said parameter indicative of the level of said morphogen is determined using a nucleic acid probe that hybridizes under stringent conditions with nucleic acid encoding said morphogen.

19. The method of claim 18 wherein said morphogen comprises a minimally active core C-terminal region comprising at least six cysteine residues, and said nucleic acid probe hybridizes with an mRNA encoding a region N-terminal to said core region.

20. The method of claim 18 wherein said morphogen comprises a minimally active core C-terminal region

comprising at least six cysteine residues, and said nucleic acid probe hybridizes with an mRNA encoding a region 3' to said core region.

1 / 3

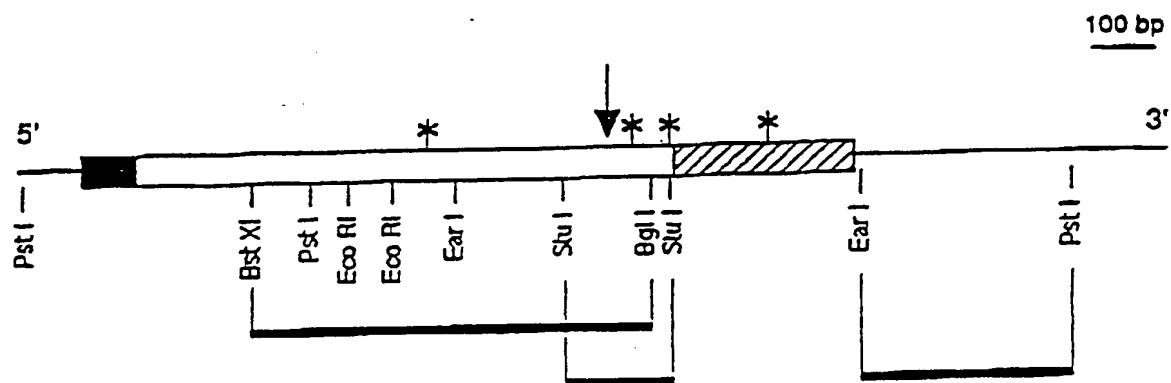


Fig 1

2 / 3

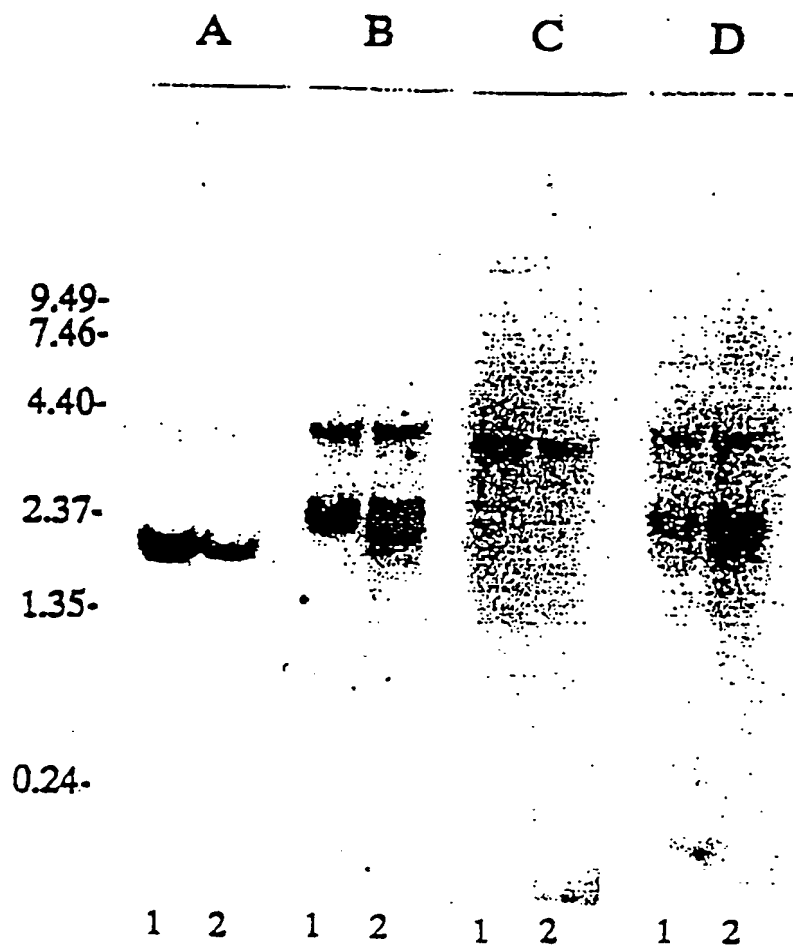


Fig 2

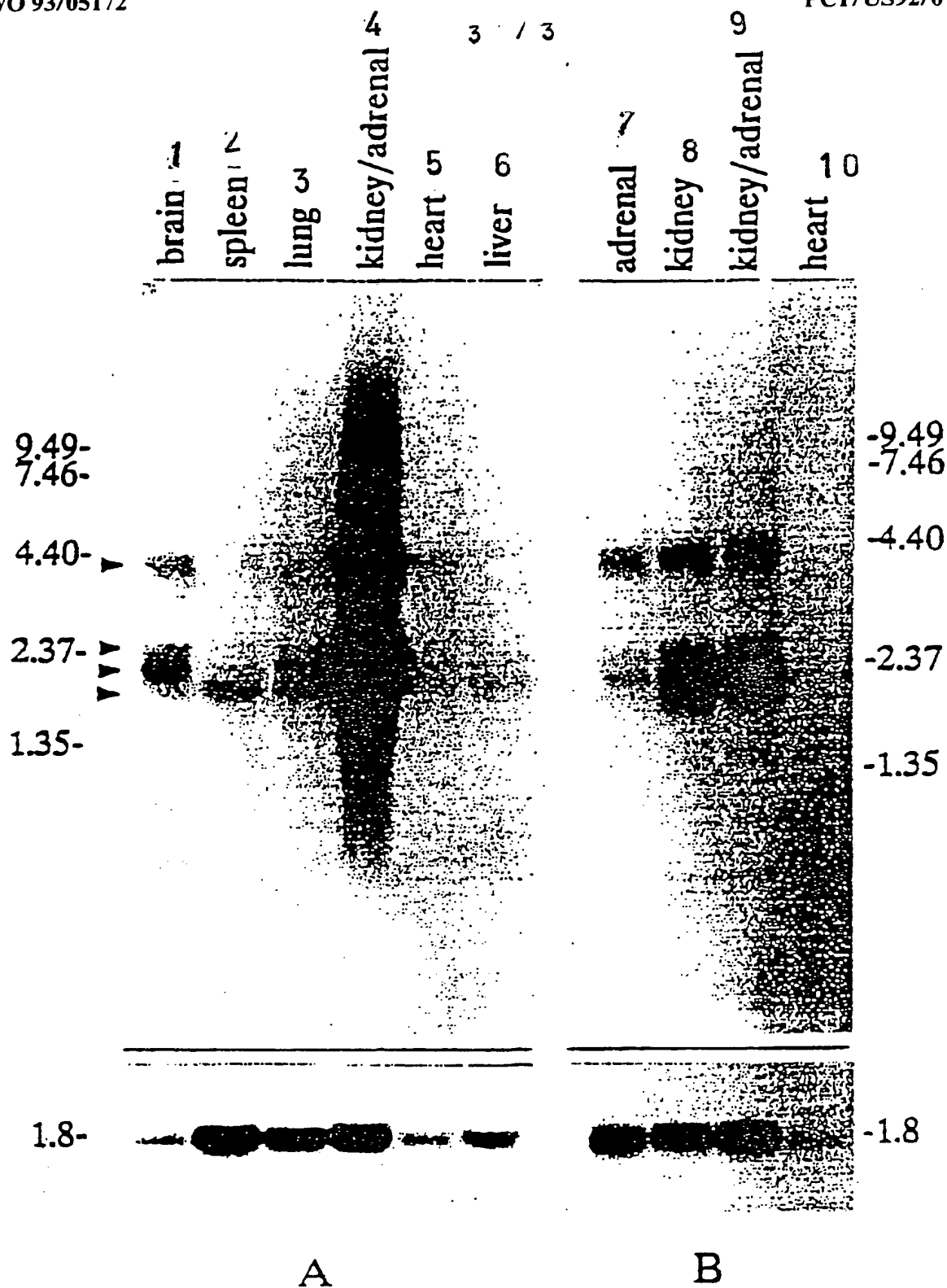


Fig 3

I. CLASSIFICATION OF SUBJECT MATTER (if several classification symbols apply, indicate all)⁶

According to International Patent Classification (IPC) or to both National Classification and IPC

Int.Cl. 5 C12Q1/02; G01N33/68

II. FIELDS SEARCHED

Minimum Documentation Searched⁷

Classification System

Classification Symbols

Int.Cl. 5

C12Q ; G01N ; C07K

Documentation Searched other than Minimum Documentation
to the Extent that such Documents are Included in the Fields Searched⁸

III. DOCUMENTS CONSIDERED TO BE RELEVANT⁹

Category ¹⁰	Citation of Document, ¹¹ with indication, where appropriate, of the relevant passages ¹²	Relevant to Claim No. ¹³
X	JOURNAL OF BONE AND MINERAL RESEARCH vol. 6, no. 7, July 1991, pages 767 - 777 H.ZHOU ET AL.	1, 15, 18
Y	see abstract see page 768, left column, line 22 - line 55 see page 771, right column, line 12 - page 772, left column, line 8 see page 774, right column, line 4 - line 44 --- -/--	6

¹⁰ Special categories of cited documents:

- "A" document defining the general state of the art which is not considered to be of particular relevance
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IV. CERTIFICATION

Date of the Actual Completion of the International Search

09 DECEMBER 1992

Date of Mailing of this International Search Report

13. 01. 93

International Searching Authority

EUROPEAN PATENT OFFICE

Signature of Authorized Officer

LUZZATTO E.R.

III. DOCUMENTS CONSIDERED TO BE RELEVANT (CONTINUED FROM THE SECOND SHEET)

Category *	Citation of Document, with indication, where appropriate, of the relevant passages	Relevant to Claims No.
X	<p>PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA. vol. 86, June 1989, WASHINGTON US pages 4554 - 4558 K.LYONS ET AL. cited in the application see abstract see page 4557, left column, line 34 - page 4558, line 18; figure 5</p> <p>---</p>	1,11,15,19
X	<p>WO,A,9 102 744 (CELTRIX LABORATORIES) 7 March 1991 see page 1, line 1 - page 3, line 34 see page 29, line 1 - line 28</p> <p>---</p>	15,16
Y	<p>PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA. vol. 88, May 1991, WASHINGTON US pages 4250 - 4254 S.-J. LEE see abstract</p> <p>---</p>	6
Y	<p>WO,A,9 000 619 (UNIVERSITY COLLEGE LONDON) 25 January 1990 see page 1, line 1 - page 2, line 18 see page 4, line 14 - page 14, line 10</p> <p>---</p>	1,15
P,Y	<p>BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS. vol. 179, no. 1, 30 August 1991, DULUTH, MINNESOTA US pages 116 - 123 E. ÖZKAYANAK ET AL. see the whole document</p> <p>-----</p>	1,15

**ANNEX TO THE INTERNATIONAL SEARCH REPORT
ON INTERNATIONAL PATENT APPLICATION NO.**

US 9207359
SA 64596

This annex lists the patent family members relating to the patent documents cited in the above-mentioned international search report. The members are as contained in the European Patent Office EDP file on
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Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO-A-9102744	07-03-91	AU-A- 6187090	03-04-91
		CA-A- 2064878	22-02-91
		EP-A- 0489062	10-06-92

WO-A-9000619	25-01-90	JP-T- 3505669	12-12-91

EP FORM P0479



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

<p>(51) International Patent Classification⁵ : C12Q 1/02, G01N 33/68</p>	<p>A1</p>	<p>(11) International Publication Number: WO 93/05172 (43) International Publication Date: 18 March 1993 (18.03.93)</p>
<p>(21) International Application Number: PCT/US92/07359 (22) International Filing Date: 28 August 1992 (28.08.92) (30) Priority data: 752,861 30 August 1991 (30.08.91) US (71) Applicant: CREATIVE BIOMOLECULES, INC. [US/ US]; 35 South Street, Hopkinton, MA 01748 (US). (72) Inventors: SMART, John, E. ; 50 Meadow Brook Road, Weston, MA 02193 (US). OPPERMANN, Hermann ; 25 Summer Hill Road, Medway, MA 02053 (US). OZKAY- NAK, Engin ; 44 Purdue Drive, Milford, MA 01757 (US). KUBERASAMPATH, Thangavel ; 6 Spring Street, Medway, MA 02053 (US). RUEGER, David, C. ; 19 Downey Street, Hopkinton, MA 01748 (US). PANG, Roy, H., L. ; 15 Partridge Road, Etna, NH 03750 (US). COHEN, Charles, N. ; 98 Wintrop Street, Medway, MA 02053 (US).</p>		<p>(74) Agent: KELLEY, Robin, D.; Testa, Hurwitz & Thibault, 53 State Street/Exchange Place, Boston, MA 02018-2809 (US). (81) Designated States: AU, CA, JP, European patent (AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, SE). Published <i>With international search report. Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i></p>
<p>(54) Title: MORPHOGENIC PROTEIN SCREENING METHOD (57) Abstract Disclosed is a method of screening candidate compounds for the ability to modulate the level of morphogenic protein in mammalian system. The method includes determining a parameter indicative of the level of production of a morphogenic in a cell culture known to produce the morphogen, incubating a candidate compound with the culture for a time sufficient to allow the compound to affect the production of the morphogenic protein, and then assaying the culture again to detect a change in the level of morphogenic protein production.</p>		

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AT	Austria	FR	France	MR	Mauritania
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FI	Finland				

MORPHOGENIC PROTEIN SCREENING METHOD

The invention relates to a method of screening drugs for the ability to modulate the level in mammals of proteins which can induce tissue morphogenesis and to methods of determining which animal tissue(s) and/or cell types within a tissue express a particular morphogenic protein.

Background of the Invention

Cell differentiation is the central characteristic of morphogenesis which initiates in the embryo, and continues to various degrees throughout the life of an organism in adult tissue repair and regeneration mechanisms. Members of the TGF- β superfamily include subfamilies of highly-related genes that now are suspected to play important roles in cell differentiation and morphogenesis during development and/or during adult life. For example, the *Drosophila* decapentaplegic gene product (DPP) has been implicated in formation of the dorsal-ventral axis in fruit flies; activins induce mesoderm and anterior structure formation in mammals; Müllerian inhibiting substance (MIS) may be required for male sex development in mammals; growth/differentiation factor-1 (GDF-1) has been implicated in nerve development and maintenance; other morphogenic proteins (BMP-2, -3, -4 and OP-1) induce bone formation.

The development and study of a bone induction model system has identified the developmental cascade of bone differentiation as consisting of chemotaxis of mesenchymal cells, proliferation of these progenitor cells, differentiation of cartilage, ossification and hypertrophy of this cartilaginous tissue, vascular invasion, bone formation, remodeling, and finally, marrow differentiation (Reddi (1981) Collagen Rel. Res. 1:209-206). This bone model system, which is studied in adult mammals, recapitulates the cascade of bone differentiation events that occur in formation of bone in the developing fetus. In other studies, the epithelium of the urinary bladder has been shown to induce new bone formation. Huggins (1931, Arch. Surg. 22:377-408) showed that new bone formation could be induced by surgical transplantation of urinary bladder epithelium onto the parietal fascia. Urist (1965, Science 150:893-899) demonstrated that implantation of demineralized bone segments resulted in endochondral bone formation. The latter study and observation suggested the existence of an osteogenic protein and that bovine diaphyseal bone was a source of enriched preparations of osteogenic protein (Sampath et al., J. Biol. Chem. 265:13198-13205, 1990; Urist, *ibid*; Reddi et al., Proc. Nat. Aca. Sci. 69:1601-1605, 1972; Sampath et al., Proc. Natl. Acad. Sci. 80:6591-6595, 1983). Proteins capable of inducing endochondral bone formation in mammals when implanted in association with a matrix now have been identified in a number of different mammalian species, as have the genes encoding these proteins, (see, for example, U.S. Patent No. 4,968,590; U.S.S.N. 315,342 filed February 23, 1989;

and U.S.S.N. 599,543, filed October 18, 1990). Human OP-1 DNA has been cloned from various cDNA and genomic libraries using a consensus probe (Ozkaynak et al., EMBO J. 9:2085-2093, 1990). Purified human recombinant OP-1, expressed in mammalian cells, has been shown to induce new bone formation in vivo. Like other members of the TGF- β superfamily, OP-1 is produced as a precursor, glycosylated, processed and secreted as a mature dimer. Mature OP-1 is cleaved at a maturation site following a sequence with the pattern of RXXR (Panganiban et al., Mol. Cell. Biol. 10:2669-2677, 1990).

The degree of morphogenesis in adult tissue varies among different tissues and depends on, among other factors, the degree of cell turnover in a given tissue. On this basis, tissues can be divided into three broad categories: 1) tissues with static cell populations such as nerve and skeletal muscle where there is little or no cell division and most of the cells formed during development persist throughout adult life and, therefore, possess little or no ability for normal regeneration after injury; 2) tissues containing conditionally renewing populations such as liver where there is generally little cell division but, in response to an appropriate stimulus or injury, cells can divide to produce daughters of the same differentiated cell type; and 3) tissues with permanently renewing populations including blood, bone, testes, and stratified squamous epithelia which are characterized by rapid and continuous cell turnover in the adult. Here, the terminally differentiated cells have a short life span and are replaced through

proliferation of a distinct subpopulation of cells, known as stem or progenitor cells.

It is an object of this invention to provide a method of screening compounds which, when administered to a given tissue from a given organism, cause an alteration in the level of morphogenic protein ("morphogen") produced by the tissue. Such compounds, when administered systemically, will result in altered systemic or local levels of morphogenic activity. This morphogenic activity includes the ability to induce proliferation and sequential differentiation of progenitor cells, and the ability to support and maintain the differentiated phenotype or sequence of phenotypes through the progression of events that results in the formation of normal adult tissue (including organ regeneration). Thus, broadly, the invention provides a key to development of additional modalities of therapies involving modulation of morphogenic protein production in animals or adult mammals, e.g., humans, and consequent correction of conditions involving pathologic alteration of the balance of tissue cell turnover. Another object of the invention is to provide methodologies for identifying or selecting a combination of compound(s) which may increase a progenitor cell population in a mammal, stimulate progenitor cells to differentiate in vivo or in vitro, maintain the differentiated phenotype or sequence of phenotypes of a tissue, induce tissue-specific growth in vivo, or replace diseased or damaged tissues or organs in vivo. Another object of the invention is to determine the tissue(s) or organ(s) of origin of a given morphogen. Another object of the

invention is to determine the specific cell type(s) within the tissue(s) or organ(s) of origin, or cell line(s) derived from the tissue(s), or organ(s) of origin, that is responsible for the synthesis and production of a given morphogen. These and other objects and features of the invention will be apparent from the description, drawing, and claims which follow.

Summary of the Invention

The invention features a method of screening candidate compounds for the ability to modulate the effective local or systemic concentration or level of morphogenic protein in an organism. The method is practiced by incubating one or more candidate compound(s) with cells from a test tissue type of an organism known to produce a given morphogen for a time sufficient to allow the compound(s) to affect the production, i.e., expression and/or secretion, of morphogen by the cells; and then assaying cells and the medium conditioned by the cells for a change in a parameter indicative of the level of production of the morphogenic protein. The procedure may be used to identify compounds showing promise as drugs for human use capable of increasing or decreasing morphogen production in vivo, thereby to correct or alleviate a diseased condition.

In a related aspect, the invention features a method of screening tissue(s) of an organism to assess whether or at what level cells of the tissue(s) produce a particular morphogen, thereby to determine a tissue(s) of origin of the morphogen. This permits selection of the tissue cell type to be used in the screening. As used herein, "tissue" refers to a group of cells which are naturally found associated, including an organ.

As an example of tissue(s) or organ(s) which produce high levels of morphogen relative to the level produced by other types of tissues, it has been discovered that OP-1, first found in bone tissue is produced at relatively high levels in cells derived

from renal, e.g., kidney or bladder, or adrenal tissue; that GDF-1 is produced at relatively high levels in cells derived from nerve, e.g., brain tissue; that DPP is produced at relatively high levels in cells derived from one of the following drosophila tissues: dorsal ectoderm, epithelial imaginal disc, visceral mesoderm, or gut endoderm; that Vgr-1 is produced at relatively high levels in cells derived from mouse lung tissue; and that Vgl is produced at relatively high levels in cells derived from xenopus fetal endoderm tissue. In addition, BMP3 and CBMP2B transcripts have been identified in abundance in lung tissue. As used herein, "derived" means the cells are the cultured tissue itself, or are a cell line whose parent cells are the tissue itself.

Preferred methods for determining the level of or a change in the level of a morphogen in a cultured cell include using an antibody specific for the morphogen, e.g., in an immunoassay such as an ELISA or radioimmunoassay; and determining the level of nucleic acid, most particularly mRNA, encoding the morphogen using a nucleic acid probe that hybridizes under stringent conditions with the morphogen RNA, such as in an RNA dot blot analysis. Where a change in the presence and/or concentration of morphogen is being determined, it will be necessary to measure and compare the levels of morphogen in the presence and absence of the candidate compound. The nucleic acid probe may be a nucleotide sequence encoding the morphogen or a fragment large enough to hybridize specifically only to RNA encoding a specific morphogen under stringent conditions. As used herein, "stringent conditions" are

defined as conditions in which non-specific hybrids will be eluted but at which specific hybrids will be maintained, i.e., incubation at 0.1X SSC (15mM NaCl, 5mM Na citrate) at 50°C for 15 minutes.

Examples of morphogens whose levels may be determined according to the invention include OP-1, OP-2, GDF-1, Vgr-1, DPP, 60A CBMP2A, CBMP2B, BMP 2, 3, 4, 5, 6, or Vgl. Thus, if an immunoassay is used to indicate the presence and/or concentration of a morphogen, an antibody specific for one of these morphogens only, and which will not detect the presence of other morphogens, will be used. Similarly, if nucleic acid hybridization is used to indicate the level of RNA encoding the morphogen, a nucleotide probe specific for one of these morphogens only will be used under hybridization conditions such that the probe should not be capable of hybridizing with RNA encoding a different morphogen. A morphogen includes an active C-terminal core region, which includes at least six cysteine residues, and a region N-terminal to the C-terminal region that is relatively non-homologous to the equivalent N-terminal regions of other morphogens. In addition, the 3' noncoding region of the mRNA is unique to each morphogen. Thus, a nucleic acid probe encoding all or a portion of the sequences N-terminal to the C-terminal core region of a morphogen, or encoding all or a portion of the sequences C-terminal to or 3' to the core region of a morphogen may be used as a probe which detects mRNA encoding that morphogen only.

"Morphogenic proteins" or "morphogens", as used herein, include naturally-occurring osteogenic proteins

capable of inducing the full developmental cascade of bone formation, as well as polypeptide chains not normally associated with bone or bone formation, but sharing substantial sequence homology with osteogenic proteins. Such proteins, as well as DNA sequences encoding them, have been isolated and characterized for a number of different species. See, for example, U.S. Patent No. 4,968,590 and U.S. Patent Number. 5,011,691, U.S. application Serial Number 1989; 422,699, filed October 17, 1989, and 600,024 and 599,543, both filed October 18, 1990; Sampath et al., (1990) J. Biol. Chem. 265:13198-13205; Ozkaynak et al. (1990) EMBO J. 9:2085-2093; and Lee, Proc. Nat. Aca. Sci. 88:4250-4254 (1991), all of which are hereby incorporated by reference. Many of these proteins subsequently were discovered to have utility beyond bone morphogenesis. See, e.g., USSN 667,274 filed March 11, 1991. The mature forms of morphogens share substantial amino acid sequence homology, especially in the C-terminal core regions of the proteins. In particular, most of the proteins share a seven-cysteine skeleton in this region, in addition to other apparently required amino acids. Table II, infra, shows the amino acid sequence homologies for nine morphogens over the carboxy terminal 102 amino acids.

Among the morphogens useful in this invention are proteins originally identified as osteogenic proteins, such as the OP-1, OP-2 and CBMP2 proteins, as well as amino acid sequence-related proteins such as DPP (from *Drosophila*), Vgl (from *Xenopus*), Vgr-1 (from mouse, see U.S. 5,011,691 to Oppermann et al.), GDF-1 (from mouse, see Lee (1991) PNAS 88:4250-4254), all of which are

presented in Table II and Seq. ID Nos.5-14), and the recently identified 60A protein (from *Drosophila*, Seq. ID No. 24, see Wharton et al. (1991) PNAS 88:9214-9218.) The members of this family, which include members of the TGF- β super-family of proteins, share substantial amino acid sequence homology in their C-terminal regions. The proteins are translated as a precursor, having an N-terminal signal peptide sequence, typically less than about 30 residues, followed by a "pro" domain that is cleaved to yield the mature sequence. The signal peptide is cleaved rapidly upon translation, at a cleavage site that can be predicted in a given sequence using the method of Von Heijne ((1986) Nucleic Acids Research 14:4683-4691.) Table I, below, describes the various morphogens identified to date, including their nomenclature as used herein, their Seq. ID references, and publication sources for the amino acid sequences for the full length proteins not included in the Seq. Listing. The disclosure of these publications is incorporated herein by reference.

TABLE I

"OP-1"	refers generically to the group of morphogenically active proteins expressed from part or all of a DNA sequence encoding OP-1 protein, including allelic and species variants thereof, e.g., human OP-1 ("hOP-1", Seq. ID No. 5, mature protein amino acid sequence), or mouse OP-1 ("mOP-1", Seq. ID No. 6, mature protein amino acid sequence.) The
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conserved seven cysteine skeleton is defined by residues 38 to 139 of Seq. ID Nos. 5 and 6. The cDNA sequences and the amino acids encoding the full length proteins are provided in Seq. ID Nos. 16 and 17 (hOP1) and Seq. ID Nos. 18 and 19 (mOP1.) The mature proteins are defined by residues 293-431 (hOP1) and 292-430 (mOP1). The "pro" regions of the proteins, cleaved to yield the mature, morphogenically active proteins are defined essentially by residues 30-292 (hOP1) and residues 30-291 (mOP1).

"OP-2"

refers generically to the group of active proteins expressed from part or all of a DNA sequence encoding OP-2 protein, including allelic and species variants thereof, e.g., human OP-2 ("hOP-2", Seq. ID No. 7, mature protein amino acid sequence) or mouse OP-2 ("mOP-2", Seq. ID No. 8, mature protein amino acid sequence). The conserved seven cysteine skeleton is defined by residues 38 to 139 of Seq. ID Nos. 7 and 8. The cDNA sequences and the amino acids encoding the full length proteins are provided in Seq. ID Nos. 20 and 21 (hOP2) and Seq. ID Nos. 22 and 23 (mOP2.) The mature proteins are defined essentially by residues 264-402 (hOP2) and 261-399 (mOP2). The "pro" regions of the proteins, cleaved to yield

the mature, morphogenically active proteins likely are defined essentially by residues 18-263 (hOP2) and residues 18-260 (mOP2). (Another cleavage site also occurs 21 residues upstream for both OP-2 proteins.)

"CBMP2" refers generically to the morphogenically active proteins expressed from a part or all of a DNA sequence encoding the CBMP2 proteins, including allelic and species variants thereof, e.g., human CBMP2A ("CBMP2A(fx)", Seq ID No. 9) or human CBMP2B DNA ("CBMP2B(fx)", Seq. ID No. 10). The amino acid sequence for the full length proteins, referred to in the literature as BMP2A and BMP2B, or BMP2 and BMP4, appear in Wozney, et al. (1988) Science 242:1528-1534. The pro domain for BMP2 (BMP2A) likely includes residues 25-248 or 25-282; the mature protein, residues 249-396 or 283-396. The pro domain for BMP4 (BMP2B) likely includes residues 25-256 or 25-292; the mature protein, residues 257-408 or 293-408.

"DPP(fx)" refers to protein sequences encoded by the *Drosophila* DPP gene and defining the conserved seven cysteine skeleton (Seq. ID No. 11). The amino acid sequence for the full length protein appears in Padgett, et al (1987) Nature 325: 81-84. The pro

domain likely extends from the signal peptide cleavage site to residue 456; the mature protein likely is defined by residues 457-588.

"Vgl(fx)" refers to protein sequences encoded by the *Xenopus Vgl* gene and defining the conserved seven cysteine skeleton (Seq. ID No. 12). The amino acid sequence for the full length protein appears in Weeks (1987) Cell 51: 861-867. The pro domain likely extends from the signal peptide cleavage site to residue 246; the mature protein likely is defined by residues 247-360.

"Vgr-1(fx)" refers to protein sequences encoded by the murine *Vgr-1* gene and defining the conserved seven cysteine skeleton (Seq. ID No. 13). The amino acid sequence for the full length protein appears in Lyons, et al, (1989) PNAS 86: 4554-4558. The pro domain likely extends from the signal peptide cleavage site to residue 299; the mature protein likely is defined by residues 300-438.

"GDF-1(fx)" refers to protein sequences encoded by the human *GDF-1* gene and defining the conserved seven cysteine skeleton (Seq. ID No. 14). The cDNA and encoded amino sequence for the full length protein is

provided in Seq. ID. No. 32. The pro domain likely extends from the signal peptide cleavage site to residue 214; the mature protein likely is defined by residues 215-372.

"60A"

refers generically to the morphogenically active proteins expressed from part or all of a DNA sequence (from the *Drosophila* 60A gene) encoding the 60A proteins (see Seq. ID No. 24 wherein the cDNA and encoded amino acid sequence for the full length protein is provided). "60A(fx)" refers to the protein sequences defining the conserved seven cysteine skeleton (residues 354 to 455 of Seq. ID No. 24.) The pro domain likely extends from the signal peptide cleavage site to residue 324; the mature protein likely is defined by residues 325-455.

"BMP3(fx)"

refers to protein sequences encoded by the human BMP3 gene and defining the conserved seven cysteine skeleton (Seq. ID No. 26). The amino acid sequence for the full length protein appears in Wozney et al. (1988) Science 242: 1528-1534. The pro domain likely extends from the signal peptide cleavage site to residue 290; the mature protein likely is defined by residues 291-472.

"BMP5(fx)" refers to protein sequences encoded by the human BMP5 gene and defining the conserved seven cysteine skeleton (Seq. ID No. 27). The amino acid sequence for the full length protein appears in Celeste, et al. (1991) PNAS 87: 9843-9847. The pro domain likely extends from the signal peptide cleavage site to residue 316; the mature protein likely is defined by residues 317-454.

"BMP6(fx)" refers to protein sequences encoded by the human BMP6 gene and defining the conserved seven cysteine skeleton (Seq. ID No. 28). The amino acid sequence for the full length protein appear sin Celeste, et al. (1990) PNAS 87: 9843-5847. The pro domain likely includes extends from the signal peptide cleavage site to residue 374; the mature sequence likely includes residues 375-513.

The OP-2 proteins have an additional cysteine residue in this region (e.g., see residue 41 of Seq. ID Nos. 7 and 8), in addition to the conserved cysteine skeleton in common with the other proteins in this family. The GDF-1 protein has a four amino acid insert within the conserved skeleton (residues 44-47 of Seq. ID No. 14) but this insert likely does not interfere with the relationship of the cysteines in the folded

structure. In addition, the CBMP2 proteins are missing one amino acid residue within the cysteine skeleton.

The morphogens are inactive when reduced, but are active as oxidized homodimers and when oxidized in combination with other morphogens of this invention. Thus, as defined herein, a morphogen is a dimeric protein comprising a pair of polypeptide chains, wherein each polypeptide chain comprises at least the C-terminal six cysteine skeleton defined by residues 43-139 of Seq. ID No. 5, including functionally equivalent arrangements of these cysteines (e.g., amino acid insertions or deletions which alter the linear arrangement of the cysteines in the sequence but not their relationship in the folded structure), such that, when the polypeptide chains are folded, the dimeric protein species comprising the pair of polypeptide chains has the appropriate three-dimensional structure, including the appropriate intra- and inter-chain disulfide bonds such that the protein is capable of acting as a morphogen as defined herein. Specifically, the morphogens generally are capable of the following biological functions in a morphogenically permissive environment: stimulating proliferation of progenitor cells; stimulating the differentiation of progenitor cells; stimulating the proliferation of differentiated cells; and supporting the growth and maintenance of differentiated cells, including the "redifferentiation" of transformed cells. In addition, it is also anticipated that these morphogens are capable of

inducing redifferentiation of committed cells under appropriate environmental conditions.

Morphogens useful in this invention comprise one of two species of generic amino acid sequences: Generic Sequence 1 (Seq. ID No. 1) or Generic Sequence 2 (Seq. ID No. 2); where each Xaa indicates one of the 20 naturally-occurring L-isomer, α -amino acids or a derivative thereof. Generic Sequence 1 comprises the conserved six cysteine skeleton and Generic Sequence 2 comprises the conserved six cysteine skeleton plus the additional cysteine identified in OP-2 (see residue 36, Seq. ID No. 2). In another preferred aspect, these sequences further comprise the following additional sequence at their N-terminus:

Cys Xaa Xaa Xaa Xaa (Seq. ID No. 15)
1 5

Preferred amino acid sequences within the foregoing generic sequences include: Generic Sequence 3 (Seq. ID No. 3), Generic Sequence 4 (Seq. ID No. 4), Generic Sequence 5 (Seq. ID No. 30) and Generic Sequence 6 (Seq. ID No. 31), listed below. These Generic Sequences accommodate the homologies shared among the various preferred members of this morphogen family identified in Table II, as well as the amino acid sequence variation among them. Specifically, Generic Sequences 3 and 4 are composite amino acid sequences of the following proteins presented in Table II and identified in Seq. ID Nos. 5-14: human OP-1 (hOP-1, Seq. ID Nos. 5 and 16-17), mouse OP-1 (mOP-1, Seq. ID

Nos. 6 and 18-19), human and mouse OP-2 (Seq. ID Nos. 7, 8, and 20-22), CBMP2A (Seq. ID No. 9), CBMP2B (Seq. ID No. 10), DPP (from *Drosophila*, Seq. ID No. 11), Vgl, (from *Xenopus*, Seq. ID No. 12), Vgr-1 (from mouse, Seq. ID No. 13), and GDF-1 (from mouse, Seq. ID No. 14.) The generic sequences include both the amino acid identity shared by the sequences in Table II, as well as alternative residues for the variable positions within the sequence. Note that these generic sequences allow for an additional cysteine at position 41 or 46 in Generic Sequences 3 or 4, respectively, providing an appropriate cysteine skeleton where inter- or intramolecular disulfide bonds can form, and contain certain critical amino acids which influence the tertiary structure of the proteins.

Generic Sequence 3

```

Leu Tyr Val Xaa Phe
      1               5
Xaa Xaa Xaa Gly Trp Xaa Xaa Trp Xaa
              10
Xaa Ala Pro Xaa Gly Xaa Xaa Ala
      15               20
Xaa Tyr Cys Xaa Gly Xaa Cys Xaa
              25               30
Xaa Pro Xaa Xaa Xaa Xaa Xaa
              35

```

Xaa Xaa Xaa Asn His Ala Xaa Xaa

40

45

Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa

50

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys

55

60

Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa

65

Xaa Xaa Xaa Leu Xaa Xaa Xaa

70

75

Xaa Xaa Xaa Xaa Val Xaa Leu Xaa

80

Xaa Xaa Xaa Xaa Met Xaa Val Xaa

85

90

Xaa Cys Gly Cys Xaa

95

wherein each Xaa is independently selected from a group of one or more specified amino acids defined as follows: "Res." means "residue" and Xaa at res.4 = (Ser, Asp or Glu); Xaa at res.6 = (Arg, Gln, Ser or Lys); Xaa at res.7 = (Asp or Glu); Xaa at res.8 = (Leu or Val); Xaa at res.11 = (Gln, Leu, Asp, His or Asn); Xaa at res.12 = (Asp, Arg or Asn); Xaa at res.14 = (Ile or Val); Xaa at res.15 = (Ile or Val); Xaa at res.18 = (Glu, Gln, Leu, Lys, Pro or Arg); Xaa at res.20 = (Tyr or Phe); Xaa at res.21 = (Ala, Ser, Asp, Met, His, Leu or Gln); Xaa at res.23 = (Tyr, Asn or Phe); Xaa at

res.26 = (Glu, His, Tyr, Asp or Gln); Xaa at res.28 = (Glu, Lys, Asp or Gln); Xaa at res.30 = (Ala, Ser, Pro or Gln); Xaa at res.31 = (Phe, Leu or Tyr); Xaa at res.33 = (Leu or Val); Xaa at res.34 = (Asn, Asp, Ala or Thr); Xaa at res.35 = (Ser, Asp, Glu, Leu or Ala); Xaa at res.36 = (Tyr, Cys, His, Ser or Ile); Xaa at res.37 = (Met, Phe, Gly or Leu); Xaa at res.38 = (Asn or Ser); Xaa at res.39 = (Ala, Ser or Gly); Xaa at res.40 = (Thr, Leu or Ser); Xaa at res.44 = (Ile or Val); Xaa at res.45 = (Val or Leu); Xaa at res.46 = (Gln or Arg); Xaa at res.47 = (Thr, Ala or Ser); Xaa at res.49 = (Val or Met); Xaa at res.50 = (His or Asn); Xaa at res.51 = (Phe, Leu, Asn, Ser, Ala or Val); Xaa at res.52 = (Ile, Met, Asn, Ala or Val); Xaa at res.53 = (Asn, Lys, Ala or Glu); Xaa at res.54 = (Pro or Ser); Xaa at res.55 = (Glu, Asp, Asn, or Gly); Xaa at res.56 = (Thr, Ala, Val, Lys, Asp, Tyr, Ser or Ala); Xaa at res.57 = (Val, Ala or Ile); Xaa at res.58 = (Pro or Asp); Xaa at res.59 = (Lys or Leu); Xaa at res.60 = (Pro or Ala); Xaa at res.63 = (Ala or Val); Xaa at res.65 = (Thr or Ala); Xaa at res.66 = (Gln, Lys, Arg or Glu); Xaa at res.67 = (Leu, Met or Val); Xaa at res.68 = (Asn, Ser or Asp); Xaa at res.69 = (Ala, Pro or Ser); Xaa at res.70 = (Ile, Thr or Val); Xaa at res.71 = (Ser or Ala); Xaa at res.72 = (Val or Met); Xaa at res.74 = (Tyr or Phe); Xaa at res.75 = (Phe, Tyr or Leu); Xaa at res.76 = (Asp or Asn); Xaa at res.77 = (Asp, Glu, Asn or Ser); Xaa at res.78 = (Ser, Gln, Asn or Tyr); Xaa at res.79 = (Ser, Asn, Asp or Glu); Xaa at res.80 = (Asn, Thr or Lys); Xaa at res.82 = (Ile or Val); Xaa at res.84 = (Lys or Arg); Xaa at res.85 = (Lys, Asn, Gln or His); Xaa at res.86 = (Tyr or His);

Xaa at res.87 = (Arg, Gln or Glu); Xaa at res.88 = (Asn, Glu or Asp); Xaa at res.90 = (Val, Thr or Ala); Xaa at res.92 = (Arg, Lys, Val, Asp or Glu); Xaa at res.93 = (Ala, Gly or Glu); and Xaa at res.97 = (His or Arg);

Generic Sequence 4

Cys	Xaa	Xaa	Xaa	Xaa	Leu	Tyr	Val	Xaa	Phe
1					5				10
Xaa	Xaa	Xaa	Gly	Trp	Xaa	Xaa	Trp	Xaa	
					15				
Xaa	Ala	Pro	Xaa	Gly	Xaa	Xaa	Ala		
20					25				
Xaa	Tyr	Cys	Xaa	Gly	Xaa	Cys	Xaa		
		30					35		
Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Xaa			
					40				
Xaa	Xaa	Xaa	Asn	His	Ala	Xaa	Xaa		
		45					50		
Xaa	Xaa	Leu	Xaa	Xaa	Xaa	Xaa	Xaa		
					55				
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys		
		60					65		
Cys	Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Xaa		
		70							
Xaa	Xaa	Xaa	Leu	Xaa	Xaa	Xaa			
75					80				
Xaa	Xaa	Xaa	Xaa	Val	Xaa	Leu	Xaa		
					85				
Xaa	Xaa	Xaa	Xaa	Met	Xaa	Val	Xaa		
90					95				

Xaa Cys Gly Cys Xaa

100

wherein each Xaa is independently selected from a group of one or more specified amino acids as defined by the following: "Res." means "residue" and Xaa at res.2 = (Lys or Arg); Xaa at res.3 = (Lys or Arg); Xaa at res.4 = (His or Arg); Xaa at res.5 = (Glu, Ser, His, Gly, Arg or Pro); Xaa at res.9 = (Ser, Asp or Glu); Xaa at res.11 = (Arg, Gln, Ser or Lys); Xaa at res.12 = (Asp or Glu); Xaa at res.13 = (Leu or Val); Xaa at res.16 = (Gln, Leu, Asp, His or Asn); Xaa at res.17 = (Asp, Arg, or Asn); Xaa at res.19 = (Ile or Val); Xaa at res.20 = (Ile or Val); Xaa at res.23 = (Glu, Gln, Leu, Lys, Pro or Arg); Xaa at res.25 = (Tyr or Phe); Xaa at res.26 = (Ala, Ser, Asp, Met, His, Leu, or Gln); Xaa at res.28 = (Tyr, Asn or Phe); Xaa at res.31 = (Glu, His, Tyr, Asp or Gln); Xaa at res.33 = Glu, Lys, Asp or Gln; Xaa at res.35 = (Ala, Ser or Pro); Xaa at res.36 = (Phe, Leu or Tyr); Xaa at res.38 = (Leu or Val); Xaa at res.39 = (Asn, Asp, Ala or Thr); Xaa at res.40 = (Ser, Asp, Glu, Leu or Ala); Xaa at res.41 = (Tyr, Cys, His, Ser or Ile); Xaa at res.42 = (Met, Phe, Gly or Leu); Xaa at res.44 = (Ala, Ser or Gly); Xaa at res.45 = (Thr, Leu or Ser); Xaa at res.49 = (Ile or Val); Xaa at res.50 = (Val or Leu); Xaa at res.51 = (Gln or Arg); Xaa at res.52 = (Thr, Ala or Ser); Xaa at res.54 = (Val or Met); Xaa at res.55 = (His or Asn); Xaa at res.56 = (Phe, Leu, Asn, Ser, Ala or Val); Xaa at res.57 = (Ile, Met, Asn, Ala or Val); Xaa at res.58 = (Asn, Lys, Ala or Glu); Xaa at res.59 = (Pro or Ser); Xaa at res.60 = (Glu, Asp, or Gly); Xaa at res.61 = (Thr, Ala, Val, Lys, Asp, Tyr, Ser or Ala); Xaa at res.62 = (Val, Ala

or Ile); Xaa at res.63 = (Pro or Asp); Xaa at res.64 = (Lys or Leu); Xaa at res.65 = (Pro or Ala); Xaa at res.68 = (Ala or Val); Xaa at res.70 = (Thr or Ala); Xaa at res.71 = (Gln, Lys, Arg or Glu); Xaa at res.72 = (Leu, Met or Val); Xaa at res.73 = (Asn, Ser or Asp); Xaa at res.74 = (Ala, Pro or Ser); Xaa at res.75 = (Ile, Thr or Val); Xaa at res.76 = (Ser or Ala); Xaa at res.77 = (Val or Met); Xaa at res.79 = (Tyr or Phe); Xaa at res.80 = (Phe, Tyr or Leu); Xaa at res.81 = (Asp or Asn); Xaa at res.82 = (Asp, Glu, Asn or Ser); Xaa at res.83 = (Ser, Gln, Asn or Tyr); Xaa at res.84 = (Ser, Asn, Asp or Glu); Xaa at res.85 = (Asn, Thr or Lys); Xaa at res.87 = (Ile or Val); Xaa at res.89 = (Lys or Arg); Xaa at res.90 = (Lys, Asn, Gln or His); Xaa at res.91 = (Tyr or His); Xaa at res.92 = (Arg, Gln or Glu); Xaa at res.93 = (Asn, Glu or Asp); Xaa at res.95 = (Val, Thr or Ala); Xaa at res.97 = (Arg, Lys, Val, Asp or Glu); Xaa at res.98 = (Ala, Gly or Glu); and Xaa at res.102 = (His or Arg).

Similarly, Generic Sequence 5 (Seq. ID No. 30) and Generic Sequence 6 (Seq. ID No. 31) accommodate the homologies shared among all the morphogen protein family members identified in Table II. Specifically, Generic Sequences 5 and 6 are composite amino acid sequences of human OP-1 (hOP-1, Seq. ID Nos. 5 and 16-17), mouse OP-1 (mOP-1, Seq. ID Nos. 6 and 18-19), human and mouse OP-2 (Seq. ID Nos. 7, 8, and 20-22), CBMP2A (Seq. ID No. 9), CBMP2B (Seq. ID No. 10), DPP (from Drosophila, Seq. ID No. 11), Vgl, (from Xenopus, Seq. ID No. 12), Vgr-1 (from mouse, Seq. ID No. 13), and GDF-1 (from mouse, Seq. ID No. 14), human BMP3

(Seq. ID No. 26), human BMP5 (Seq. ID No. 27), human BMP6 (Seq. ID No. 28) and 60(A) (from Drosophila, Seq. ID Nos. 24-25). The generic sequences include both the amino acid identity shared by these sequences in the C-terminal domain, defined by the six and seven cysteine skeletons (Generic Sequences 5 and 6, respectively), as well as alternative residues for the variable positions within the sequence. As for Generic Sequences 3 and 4, Generic Sequences 5 and 6 allow for an additional cysteine at position 41 (Generic Sequence 5) or position 46 (Generic Sequence 6), providing an appropriate cysteine skeleton where inter- or intramolecular disulfide bonds can form, and containing certain critical amino acids which influence the tertiary structure of the proteins.

Generic Sequence 5

```

Leu Xaa Xaa Xaa Phe
1                               5
Xaa Xaa Xaa Gly Trp Xaa Xaa Trp Xaa
                               10
Xaa Xaa Pro Xaa Xaa Xaa Xaa Ala
15                               20
Xaa Tyr Cys Xaa Gly Xaa Cys Xaa
                               25                               30
Xaa Pro Xaa Xaa Xaa Xaa Xaa
                               35

```

Xaa Xaa Xaa Asn His Ala Xaa Xaa

40

45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

50

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys

55

60

Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa

65

Xaa Xaa Xaa Leu Xaa Xaa Xaa

70

75

Xaa Xaa Xaa Xaa Val Xaa Leu Xaa

80

Xaa Xaa Xaa Xaa Met Xaa Val Xaa

85

90

Xaa Cys Xaa Cys Xaa

95

wherein each Xaa is independently selected from a group of one or more specified amino acids defined as follows: "Res." means "residue" and Xaa at res.2 = (Tyr or Lys); Xaa at res.3 = Val or Ile); Xaa at res.4 = (Ser, Asp or Glu); Xaa at res.6 = (Arg, Gln, Ser, Lys or Ala); Xaa at res.7 = (Asp, Glu or Lys); Xaa at res.8 = (Leu, Val or Ile); Xaa at res.11 = (Gln, Leu, Asp, His, Asn or Ser); Xaa at res.12 = (Asp, Arg, Asn or Glu); Xaa at res.14 = (Ile or Val); Xaa at res.15 = (Ile or Val); Xaa at res.16 (Ala or Ser); Xaa at res.18 = (Glu, Gln, Leu, Lys, Pro or Arg); Xaa at res.19 =

(Gly or Ser); Xaa at res.20 = (Tyr or Phe); Xaa at res.21 = (Ala, Ser, Asp, Met, His, Gln, Leu or Gly); Xaa at res.23 = (Tyr, Asn or Phe); Xaa at res.26 = (Glu, His, Tyr, Asp, Gln or Ser); Xaa at res.28 = (Glu, Lys, Asp, Gln or Ala); Xaa at res.30 = (Ala, Ser, Pro, Gln or Asn); Xaa at res.31 = (Phe, Leu or Tyr); Xaa at res.33 = (Leu, Val or Met); Xaa at res.34 = (Asn, Asp, Ala, Thr or Pro); Xaa at res.35 = (Ser, Asp, Glu, Leu, Ala or Lys); Xaa at res.36 = (Tyr, Cys, His, Ser or Ile); Xaa at res.37 = (Met, Phe, Gly or Leu); Xaa at res.38 = (Asn, Ser or Lys); Xaa at res.39 = (Ala, Ser, Gly or Pro); Xaa at res.40 = (Thr, Leu or Ser); Xaa at res.44 = (Ile, Val or Thr); Xaa at res.45 = (Val, Leu or Ile); Xaa at res.46 = (Gln or Arg); Xaa at res.47 = (Thr, Ala or Ser); Xaa at res.48 = (Leu or Ile); Xaa at res.49 = (Val or Met); Xaa at res.50 = (His, Asn or Arg); Xaa at res.51 = (Phe, Leu, Asn, Ser, Ala or Val); Xaa at res.52 = (Ile, Met, Asn, Ala, Val or Leu); Xaa at res.53 = (Asn, Lys, Ala, Glu, Gly or Phe); Xaa at res.54 = (Pro, Ser or Val); Xaa at res.55 = (Glu, Asp, Asn, Gly, Val or Lys); Xaa at res.56 = (Thr, Ala, Val, Lys, Asp, Tyr, Ser, Ala, Pro or His); Xaa at res.57 = (Val, Ala or Ile); Xaa at res.58 = (Pro or Asp); Xaa at res.59 = (Lys, Leu or Glu); Xaa at res.60 = (Pro or Ala); Xaa at res.63 = (Ala or Val); Xaa at res.65 = (Thr, Ala or Glu); Xaa at res.66 = (Gln, Lys, Arg or Glu); Xaa at res.67 = (Leu, Met or Val); Xaa at res.68 = (Asn, Ser, Asp or Gly); Xaa at res.69 = (Ala, Pro or Ser); Xaa at res.70 = (Ile, Thr, Val or Leu); Xaa at res.71 = (Ser, Ala or Pro); Xaa at res.72 = (Val, Met or Ile); Xaa at res.74 = (Tyr or Phe); Xaa at res.75 = (Phe, Tyr, Leu or His); Xaa at res.76 = (Asp, Asn or

Leu); Xaa at res.77 = (Asp, Glu, Asn or Ser); Xaa at res.78 = (Ser, Gln, Asn, Tyr or Asp); Xaa at res.79 = (Ser, Asn, Asp, Glu or Lys); Xaa at res.80 = (Asn, Thr or Lys); Xaa at res.82 = (Ile, Val or Asn); Xaa at res.84 = (Lys or Arg); Xaa at res.85 = (Lys, Asn, Gln, His or Val); Xaa at res.86 = (Tyr or His); Xaa at res.87 = (Arg, Gln, Glu or Pro); Xaa at res.88 = (Asn, Glu or Asp); Xaa at res.90 = (Val, Thr, Ala or Ile); Xaa at res.92 = (Arg, Lys, Val, Asp or Glu); Xaa at res.93 = (Ala, Gly, Glu or Ser); Xaa at res.95 = (Gly or Ala) and Xaa at res.97 = (His or Arg).

Generic Sequence 6

Cys	Xaa	Xaa	Xaa	Xaa	Leu	Xaa	Xaa	Xaa	Phe		
1				5					10		
Xaa	Xaa	Xaa	Gly	Trp	Xaa	Xaa	Trp	Xaa			
			15								
Xaa	Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Ala				
20				25							
Xaa	Tyr	Cys	Xaa	Gly	Xaa	Cys	Xaa				
		30					35				
Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Xaa					
			40								
Xaa	Xaa	Xaa	Asn	His	Ala	Xaa	Xaa				
		45					50				
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa			
			55								
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys			
		60					65				
Cys	Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Xaa				
			70								

```

Xaa Xaa Xaa Leu Xaa Xaa Xaa
 75                               80
Xaa Xaa Xaa Xaa Val Xaa Leu Xaa
                        85
Xaa Xaa Xaa Xaa Met Xaa Val Xaa
 90                               95
Xaa Cys Xaa Cys Xaa
                100

```

wherein each Xaa is independently selected from a group of one or more specified amino acids as defined by the following: "Res." means "residue" and Xaa at res.2 = (Lys, Arg, Ala or Gln); Xaa at res.3 = (Lys, Arg or Met); Xaa at res.4 = (His, Arg or Gln); Xaa at res.5 = (Glu, Ser, His, Gly, Arg, Pro, Thr, or Tyr); Xaa at res.7 = (Tyr or Lys); Xaa at res.8 = (Val or Ile); Xaa at res.9 = (Ser, Asp or Glu); Xaa at res.11 = (Arg, Gln, Ser, Lys or Ala); Xaa at res.12 = (Asp, Glu, or Lys); Xaa at res.13 = (Leu, Val or Ile); Xaa at res.16 = (Gln, Leu, Asp, His, Asn or Ser); Xaa at res.17 = (Asp, Arg, Asn or Glu); Xaa at res.19 = (Ile or Val); Xaa at res.20 = (Ile or Val); Xaa at res.21 = (Ala or Ser); Xaa at res.23 = (Glu, Gln, Leu, Lys, Pro or Arg); Xaa at res.24 = (Gly or Ser); Xaa at res.25 = (Tyr or Phe); Xaa at res.26 = (Ala, Ser, Asp, Met, His, Gln, Leu, or Gly); Xaa at res.28 = (Tyr, Asn or Phe); Xaa at res.31 = (Glu, His, Tyr, Asp, Gln or Ser); Xaa at res.33 = Glu, Lys, Asp, Gln or Ala); Xaa at res.35 = (Ala, Ser, Pro, Gln or Asn); Xaa at res.36 = (Phe, Leu or Tyr); Xaa at res.38 = (Leu, Val or Met); Xaa at res.39 = (Asn, Asp, Ala, Thr or Pro); Xaa at res.40 = (Ser, Asp, Glu, Leu, Ala or Lys); Xaa at res.41 = (Tyr,

Cys, His, Ser or Ile); Xaa at res.42 = (Met, Phe, Gly or Leu); Xaa at res.43 = (Asn, Ser or Lys); Xaa at res.44 = (Ala, Ser, Gly or Ile); Xaa at res.45 = (Thr, Leu or Ser); Xaa at res.49 = (Ile, Val or Thr); Xaa at res.50 = (Val, Leu or Ile); Xaa at res.51 = (Gln or Arg); Xaa at res.52 = (Thr, Ala or Ser); Xaa at res.53 = (Leu or Ile); Xaa at res.54 = (Val or Met); Xaa at res.55 = (His, Asn or Val); Xaa at res.56 = (Phe, Leu, Asn, Ser, Ala or Val); Xaa at res.57 = (Ile, Met, Asn, Ala, Val or Leu); Xaa at res.58 = (Pro, Ser or Val); Xaa at res.59 = (Glu, Asp, Gly, Val or Lys); Xaa at res.60 = (Thr, Ala, Val, Lys, Asp, Tyr, Ser, Ala, Pro or His); Xaa at res.61 = (Val, Ala or Val); Xaa at res.62 = (Val, Ala or Ile); Xaa at res.63 = (Pro or Asp); Xaa at res.64 = (Lys, Leu or Glu); Xaa at res.65 = (Pro or Ala); Xaa at res.66 = (Ala or Val); Xaa at res.67 = (Thr, Ala or Glu); Xaa at res.68 = (Ala or Val); Xaa at res.69 = (Gln, Lys, Arg or Glu); Xaa at res.70 = (Leu, Met or Val); Xaa at res.71 = (Ala, Pro or Ser); Xaa at res.72 = (Ile, Thr, Val or Leu); Xaa at res.73 = (Ser, Ala or Pro); Xaa at res.74 = (Val, Met or Ile); Xaa at res.75 = (Tyr or Phe); Xaa at res.76 = (Phe, Tyr, Leu or His); Xaa at res.77 = (Asp, Asn or Leu); Xaa at res.78 = (Asp, Glu, Asn or Ser); Xaa at res.79 = (Ser, Gln, Asp, Glu or Lys); Xaa at res.80 = (Ser, Asn, Asp, Glu or Lys); Xaa at res.81 = (Lys, Asn, Gln, His or Val); Xaa at res.82 = (Ile, Tyr or His); Xaa at res.83 = (Arg, Gln, Glu or Pro); Xaa at res.84 = (Asn, Glu or Asp); Xaa at res.85 = (Val, Thr, Ala or Ile); Xaa at res.86 = (Arg, Lys, Val, Val, Thr, Ala or Ile); Xaa at res.87 = (Arg, Lys, Val, Val, Thr, Ala or Ile); Xaa at res.88 = (Arg, Lys, Val, Val, Thr, Ala or Ile); Xaa at res.89 = (Arg, Lys, Val, Val, Thr, Ala or Ile); Xaa at res.90 = (Arg, Lys, Val, Val, Thr, Ala or Ile); Xaa at res.91 = (Arg, Lys, Val, Val, Thr, Ala or Ile); Xaa at res.92 = (Arg, Lys, Val, Val, Thr, Ala or Ile); Xaa at res.93 = (Arg, Lys, Val, Val, Thr, Ala or Ile); Xaa at res.94 = (Arg, Lys, Val, Val, Thr, Ala or Ile); Xaa at res.95 = (Arg, Lys, Val, Val, Thr, Ala or Ile); Xaa at res.96 = (Arg, Lys, Val, Val, Thr, Ala or Ile); Xaa at res.97 = (Arg, Lys, Val, Val, Thr, Ala or Ile); Xaa at res.98 = (Arg, Lys, Val, Val, Thr, Ala or Ile); Xaa at res.99 = (Arg, Lys, Val, Val, Thr, Ala or Ile); Xaa at res.100 = (Arg, Lys, Val, Val, Thr, Ala or Ile);

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Asp or Glu); Xaa at res.98 = (Ala, Gly, Glu or Ser);
Xaa at res.100 = (Gly or Ala); and Xaa at res.102 =
(His or Arg).

Particularly useful sequences for use as morphogens in this invention include the C-terminal domains, e.g., the C-terminal 96-102 amino acid residues of Vgl, Vgr-1, DPP, OP-1, OP-2, CBMP-2A, CBMP-2B, GDF-1 (see Table II, below, and Seq. ID Nos. 5-14), as well as proteins comprising the C-terminal domains of 60A, BMP3, BMP5 and BMP6 (see Seq. ID Nos. 24-28), all of which include at least the conserved six or seven cysteine skeleton. In addition, biosynthetic constructs designed from the generic sequences, such as COP-1, 3-5, 7, 16, disclosed in U.S. Pat. No. 5,011,691, also are useful. Other sequences include the inhibins/activin proteins (see, for example, U.S. Pat. Nos. 4,968,590 and 5,011,691). Accordingly, other useful sequences are those sharing at least 70% amino acid sequence homology or "similarity", and preferably 80% homology or similarity with any of the sequences above. These are anticipated to include allelic and species variants and mutants, and biosynthetic muteins, as well as novel members of this morphogenic family of proteins. Particularly envisioned in the family of related proteins are those proteins exhibiting morphogenic activity and wherein the amino acid changes from the preferred sequences include conservative changes, e.g., those as defined by Dayoff et al., Atlas of Protein Sequence and Structure; vol. 5, Suppl. 3, pp. 345-362, (M.O. Dayoff, ed., Nat'l BioMed. Research Fdn., Washington, D.C. 1979). As used

herein, potentially useful sequences are aligned with a known morphogen sequence using the method of Needleman et al. ((1970) J.Mol.Biol. 48:443-453) and identities calculated by the Align program (DNASTar, Inc.). "Homology" or "similarity" as used herein includes allowed conservative changes as defined by Dayoff et al.

Morphogen sequences which are detectable according to the methods of the invention include but are not limited to those having greater than 60% identity, preferably greater than 65% identity, with the amino acid sequence defining the conserved six cysteine skeleton of hOP1 (e.g., residues 43-139 of Seq. ID No. 5). These most preferred sequences include both allelic and species variants of the OP-1 and OP-2 proteins, including the Drosophila 60A protein. Accordingly, morphogens which are detectable according to the invention include active proteins comprising species of polypeptide chains having the generic amino acid sequence herein referred to as "OPX", which accommodates the homologies between the various identified species of OP1 and OP2 (Seq. ID No. 29).

The morphogens detectable in the methods of this invention include proteins comprising any of the polypeptide chains described above, whether isolated from naturally-occurring sources, or produced by recombinant DNA or other synthetic techniques, and includes allelic and species variants of these proteins, naturally-occurring or biosynthetic mutants thereof, chimeric variants containing a domain(s) or

region(s) of one family member functionally arranged with another domain(s) or regions(s) of a second family member, as well as various truncated and fusion constructs. Deletion or insertion or addition mutants also are envisioned to be active, including those which may alter the conserved C-terminal cysteine skeleton, provided that the alteration does not functionally disrupt the relationship of these cysteines in the folded structure. Accordingly, such active forms are considered the equivalent of the specifically described constructs disclosed herein. The proteins may include forms having varying glycosylation patterns, varying N-termini, a family of related proteins having regions of amino acid sequence homology, and active truncated or mutated forms of native or biosynthetic proteins, produced by expression of recombinant DNA in host cells.

The morphogenic proteins can be expressed from intact or truncated cDNA or from synthetic DNAs in procaryotic or eucaryotic host cells, and purified, cleaved, refolded, and dimerized to form morphogenically active compositions. Currently preferred host cells include E. coli or mammalian cells, such as CHO, COS or BSC cells. A detailed description of the morphogens detectable according to the methods of this invention is disclosed in copending US patent application Serial Nos. 752,764, filed August 30, 1991, and 667,274, filed March 11, 1991, the disclosure of which are incorporated herein by reference.

The screening method of the invention provides a simple method of determining a change in the level of morphogenic protein as a result of exposure of cultured cells to one or more compound(s). The level of a morphogenic protein in a given cell culture, or a change in that level resulting from exposure to one or more compound(s) indicates the level of the morphogen expressed by the cultured cells. If, for example, a compound upregulated the production of OP-1 by a kidney cell line, it would then be desirable to test systemic administration of this compound in an animal model to determine if it upregulated the production of OP-1 in vivo. If this compound did upregulate the endogenous circulating levels of OP-1, it would be consistent with administration of the compound systemically for the purpose of correcting bone metabolism diseases such as osteoporosis. The level of morphogen in the body may be a result of a wide range of physical conditions, e.g., tissue degeneration such as occurs in diseases including arthritis, emphysema, osteoporosis, kidney diseases, lung diseases, cardiomyopathy, and cirrhosis of the liver. The level of morphogens in the body may also occur as a result of the normal process of aging. A compound selected by the screening method of the invention as, for example, one which increases the level of morphogen in a tissue, may be consistent with the administration of the compound systemically or locally to a tissue for the purpose of preventing the form of tissue degeneration or for restoring some degenerated tissue to its normal healthy level.

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Other advantages of the invention include determining the tissue or tissues of origin of a given morphogen in order to administer a compound aimed at modulating the systemic level of morphogen for treatment of a disease or condition in which the level of morphogen production has become altered.

Brief Description of the Drawings

Fig. 1 shows the fragments of OP-1, used as probes in Northern hybridizations useful in the processes of the invention.

Fig. 2 shows results of Northern blot analysis of RNA using different OP-1-specific probes.

Fig. 3 shows results of Northern blot analysis of RNA from different cells types probed with an OP-1 probe.

Detailed Description

The invention is based on the discovery of a family of structurally related morphogenic proteins (BMPs), also called osteogenic proteins (OPs), and more particularly that various of these proteins play an important role, not only in embryogenesis, but also in tissue and organ maintenance and repair in juvenile and adult mammals. Morphogenic proteins which have been identified include BMP 2, 3, 4, 5, 6, OP-1 and OP-2 (murine and human), Vgr-1, Vgl, DPP, GDF-1, CMBP-2A, CMBP-2B, 60A, and the inhibin/activin class of proteins. Other recombinant proteins include COP1, COP3, COP4, COP5, COP7, and COP16. While, as explained herein, the morphogen have significant homologies and similarities in structure, it is hypothesized that variants within the morphogenic protein genes may have specific roles in specific tissue involving, for example, stimulation of progenitor cell multiplication, tissue specific or tissue preferred phenotype maintenance, and/or stimulation or modulation of the rate of differentiation, growth or replication of tissue cells characterized by high turnover. The effect on the long-term physiology, maintenance and repair of particular tissues by particular species of the morphogens is currently unknown in any significant detail. However, methods useful in determining which particular tissues express which particular morphogen(s), and for finding changes which stimulate or depress morphogen expression in vivo, would enable discovery and development of strategies for therapeutic treatment of a large number of diseased states, and provide drugs designed to implement the strategy.

This invention provides such methods and, more specifically, two generic processes for obtaining data which ultimately will permit determination of structure/activity relationships of specific naturally occurring mammalian morphogens and drugs capable of modulating their production. For example, using the assay of the invention, it has been determined that OP-1, first found in bone and demonstrated to be osteoinductive, is synthesized primarily in kidney, bladder, and adrenal tissue. This surprising discovery, coupled with the observation that patients with kidney disease often express loss of bone mass, suggests that the bone loss in these patients may be due to pathologic depression of OP-1 synthesis in kidney, and suggests that administration of OP-1 systemically or stimulation of OP-1 expression and secretion by the kidney may arrest bone loss, or effect remineralization through increased bone formation (i.e., osteogenesis).

There are two fundamental aspects of the invention. One aspect involves an assay to determine tissues and cell types capable of synthesis and secretion of the morphogens; the other involves the use of the identified cell types configured in a screening system to find substances useful therapeutically to modulate, i.e., stimulate or depress, morphogen expression and/or secretion.

The assay to determine the tissue of origin of a given morphogen involves screening a plurality (i.e., two or more) different tissues by determining a parameter indicative of production of a morphogen in the tissue, and comparing the parameters. The tissue(s) of origin will, of course, be the tissue that produces that morphogen.

The other assay of the invention involves screening candidate compounds for their ability to modulate the effective systemic or local concentration of a morphogen by incubating the compound with a cell culture that produces the morphogen, and assaying the culture for a parameter indicative of a change in the production level of the morphogen. Useful candidate compounds then may be tested for in vivo efficacy in a suitable animal model. These compounds then may be used in vivo to modulate effective morphogen concentrating in the disease treatment.

1. Morphogen Tissue Distribution

Morphogens are broadly distributed in developing and adult tissue. For example, DPP and 60A are expressed in both embryonic and developing *Drosophila* tissue. Vgl has been identified in *Xenopus* embryonic tissue. Vgr-1 transcripts have been identified in a variety of murine tissues, including embryonic and developing brain, lung, liver, kidney and calvaria (dermal bone) tissue. In addition, both CBMP2B and CBMP3 have been identified in lung tissue. Recently, Vgr-1 transcripts also have been identified in adult murine lung, kidney, heart, and brain tissue, with particularly high levels in the lung (see *infra*). GDF-1 has been identified in human adult cerebellum and in fetal brain tissue. In addition, recent Northern blot analyses indicate that OP-1 is encoded by multiple transcripts in different tissues. This potential alternative splicing is consistent with the hypothesis that the longer transcripts may encoded additional proteins (e.g., bicistronic mRNA) and each form may be tissue or developmentally related.

OP-1 and the CBMP2 proteins, both first identified as bone morphogens, have been identified in mouse and human placenta, hippocampus, calvaria and osteosarcoma tissue as determined by identification of OP-1 and CMBP2-specific sequences in cDNA libraries constructed from these tissues (see USSN 422,699, incorporated herein by reference). Additionally, the OP-1 protein is present in a variety of embryonic and developing tissues including kidney, liver, heart and brain as determined by Western blot analysis and immunolocalization (see *infra*). OP-1-specific transcripts also have been identified in both embryonic and developing tissues, most abundantly in developing kidney, bladder, adrenal and (see *infra*). OP-1 also has been identified as a mesoderm inducing factor present during embryogenesis. Moreover, OP-1 has been shown to be associated with satellite cells in the muscle and associated with potential pluripotential stem cells in bone marrow following damage to adult murine endochondral bone, indicating its morphogenic role in tissue repair and regeneration. In addition, a novel protein GDF-1 comprising a 7 cysteine skeleton, has been identified in neural tissue (Lee, 1991, *Proc. Nat. Aca. Sci.* 88: 4250-4254).

Knowledge of the tissue distribution of a given morphogen may be useful in choosing a cell type for screening according to the invention, or for targeting that cell type or tissue type for treatment. The proteins (or their mRNA transcripts) are readily identified in different tissues using standard methodologies and minor modifications thereof in tissues where expression may be low. For example, protein distribution may be determined using standard Western blot analysis or immunocytochemical techniques, and antibodies specific to the morphogen or

morphogens of interest. Similarly, the distribution of morphogen transcripts may be determined using standard Northern hybridization protocols and a transcript-specific probe and hybridization conditions.

2. Useful Morphogens

As defined herein a protein is morphogenic if it is capable of inducing the developmental cascade of cellular and molecular events that culminate in the formation of new, organ-specific tissue and comprises at least the conserved C-terminal six cysteine skeleton or its functional equivalent (see supra). Specifically, the morphogens generally are capable of, all of the following biological functions in a morphogenically permissive environment: stimulating proliferation of progenitor cells; stimulating the differentiation of progenitor cells; stimulating the proliferation of differentiated cells; and supporting the growth and maintenance of differentiated cells, including the "redifferentiation" of transformed cells. Details of how the morphogens detectable according to the methods of this invention first were identified, as well as a description on how to make, use and test them for morphogenic activity are disclosed in USSN 667,274, filed March 11, 1991 and USSN 752,764, filed August 30, 1991, the disclosures of which are hereby incorporated by reference. As disclosed therein, the morphogens may be purified from naturally-sourced material or recombinantly produced from procaryotic or eucaryotic host cells, using the genetic sequences disclosed therein. Alternatively, novel morphogenic sequences may be identified following the procedures disclosed therein.

Particularly useful proteins include those which comprise the naturally derived sequences disclosed in Table II. Other useful sequences include biosynthetic constructs such as those disclosed in U.S. Pat. 5,011,691, the disclosure of which is incorporated herein by reference (e.g., COP-1, COP-3, COP-4, COP-5, COP-7, and COP-16).

Accordingly, the morphogens detectable according to the methods and compositions of this invention also may be described by morphogenically active proteins having amino acid sequences sharing 70% or, preferably, 80% homology (similarity) with any of the sequences described above, where "homology" is as defined herein above.

The morphogens detectable according to the method of this invention also can be described by any of the 6 generic sequences described herein (Generic Sequences 1, 2, 3, 4, 5 and 6). Generic sequences 1 and 2 also may include, at their N-terminus, the sequence

Cys Xaa Xaa Xaa Xaa (Seq. ID No. 15)

1

5

Table II, set forth below, compares the amino acid sequences of the active regions of native proteins that have been identified as morphogens, including human OP-1 (hOP-1, Seq. ID Nos. 5 and 16-17), mouse OP-1 (mOP-1, Seq. ID Nos. 6 and 18-19), human and mouse OP-2 (Seq. ID Nos. 7, 8, and 20-23), CBMP2A (Seq. ID No. 9), CBMP2B (Seq. ID No. 10), BMP3 (Seq. ID No. 26), DPP (from Drosophila, Seq. ID No. 11), Vgl, (from Xenopus, Seq. ID No. 12), Vgr-1 (from mouse, Seq. ID No. 13), GDF-1 (from mouse, Seq. ID

Nos. 14, 32 and 33), 60A protein (from *Drosophila*, Seq. ID Nos. 24 and 25), BMP5 (Seq. ID No. 27) and BMP6 (Seq. ID No. 28). The sequences are aligned essentially following the method of Needleman et al. (1970) J. Mol. Biol., 48:443-453, calculated using the Align Program (DNASTar, Inc.) In the table, three dots indicates that the amino acid in that position is the same as the amino acid in hOP-1. Three dashes indicates that no amino acid is present in that position, and are included for purposes of illustrating homologies. For example, amino acid residue 60 of CBMP-2A and CBMP-2B is "missing". Of course, both these amino acid sequences in this region comprise Asn-Ser (residues 58, 59), with CBMP-2A then comprising Lys and Ile, whereas CBMP-2B comprises Ser and Ile.

TABLE II

hOP-1	Cys	Lys	Lys	His	Glu	Leu	Tyr	Val
mOP-1
hOP-2	...	Arg	Arg
mOP-2	...	Arg	Arg
DPP	...	Arg	Arg	...	Ser
Vgl	Lys	Arg	His
Vgr-1	Gly
CBMP-2A	Arg	...	Pro
CBMP-2B	...	Arg	Arg	...	Ser
BMP3	...	Ala	Arg	Arg	Tyr	...	Lys	...
GDF-1	...	Arg	Ala	Arg	Arg
60A	...	Gln	Met	Glu	Thr
BMP5
BMP6	...	Arg
	1				5			

hOP-1	Ser	Phe	Arg	Asp	Leu	Gly	Trp	Gln	Asp
mOP-1
hOP-2	Gln	Leu	...
mOP-2	Ser	Leu	...
DPP	Asp	...	Ser	...	Val	Asp	...
Vgl	Glu	...	Lys	...	Val	Asn
Vgr-1	Gln	...	Val
CBMP-2A	Asp	...	Ser	...	Val	Asn	...
CBMP-2B	Asp	...	Ser	...	Val	Asn	...
BMP3	Asp	...	Ala	...	Ile	Ser	Glu
GDF-1	Glu	Val	His	Arg
60A	Asp	...	Lys	His	...

BMP5
BMP6	Gln
		10					15		

45

hOP-1	Trp	Ile	Ile	Ala	Pro	Glu	Gly	Tyr	Ala
mOP-1
hOP-2	...	Val	Gln	Ser
mOP-2	...	Val	Gln	Ser
DPP	Val	Leu	Asp
Vgl	...	Val	Gln	Met
Vgr-1	Lys
CBMP-2A	Val	Pro	His
CBMP-2B	Val	Pro	Gln
BMP3	Ser	...	Lys	Ser	Phe	Asp
GDF-1	...	Val	Arg	...	Phe	Leu
60A	Gly
BMP5
BMP6	Lys
			20					25	

hOP-1	Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ala
mOP-1
hOP-2	Ser
mOP-2
DPP	His	...	Lys	...	Pro
Vgl	...	Asn	Tyr	Pro
Vgr-1	...	Asn	Asp	Ser
CBMP-2A	...	Phe	His	...	Glu	...	Pro
CBMP-2B	...	Phe	His	...	Asp	...	Pro
BMP3	Ser	...	Ala	...	Gln
GDF-1	...	Asn	Gln	...	Gln
60A	...	Phe	Ser	Asn
BMP5	...	Phe	Asp	Ser
BMP6	...	Asn	Asp	Ser
				30					35

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hOP-1	Phe	Pro	Leu	Asn	Ser	Tyr	Met	Asn	Ala
mOP-1
hOP-2	Asp	...	Cys
mOP-2	Asp	...	Cys
DPP	Ala	Asp	His	Phe	...	Ser
Vgl	Tyr	Thr	Glu	Ile	Leu	...	Gly
Vgr-1	Ala	His
CBMP-2A	Ala	Asp	His	Leu	...	Ser
CBMP-2B	Ala	Asp	His	Leu	...	Ser
GDF-1	Leu	...	Val	Ala	Leu	Ser	Gly	Ser**	...
BMP3	Met	Pro	Lys	Ser	Leu	Lys	Pro
60A	Ala	His
BMP5	Ala	His	Met
BMP6	Ala	His	Met

40

hOP-1	Thr	Asn	His	Ala	Ile	Val	Gln	Thr	Leu
mOP-1
hOP-2	Leu	...	Ser	...
mOP-2	Leu	...	Ser	...
DPP	Val
Vgl	Ser	Leu
Vgr-1
CBMP-2A
CBMP-2B
BMP3	Ser	Thr	Ile	...	Ser	Ile
GDF-1	Leu	Val	Leu	Arg	Ala	...
60A
BMP5
BMP6

45

50

hOP-1	Val	His	Phe	Ile	Asn	Pro	Glu	Thr	Val
mOP-1	Asp
hOP-2	...	His	Leu	Met	Lys	...	Asn	Ala	...
mOP-2	...	His	Leu	Met	Lys	...	Asp	Val	...
DPP	...	Asn	Asn	Asn	Gly	Lys	...
Vgl	Ser	...	Glu	Asp	Ile
Vgr-1	Val	Met	Tyr	...
CBMP-2A	...	Asn	Ser	Val	...	Ser	---	Lys	Ile
CBMP-2B	...	Asn	Ser	Val	...	Ser	---	Ser	Ile
BMP3	...	Arg	Ala**	Gly	Val	Val	Pro	Gly	Ile
GDF-1	Met	...	Ala	Ala	Ala	...	Gly	Ala	Ala
60A	Leu	Leu	Glu	...	Lys	Lys	...
BMP5	Leu	Met	Phe	...	Asp	His	...
BMP6	Leu	Met	Tyr	...
		55					60		

hOP-1	Pro	Lys	Pro	Cys	Cys	Ala	Pro	Thr	Gln
mOP-1
hOP-2	Ala	Lys
mOP-2	Ala	Lys
DPP	Ala	Val
Vgl	...	Leu	Val	Lys
Vgr-1	Lys
CBMP-2A	Ala	Val	Glu
CBMP-2B	Ala	Val	Glu
BMP3	...	Glu	Val	...	Glu	Lys
GDF-1	Asp	Leu	Val	...	Ala	Arg
60A	Arg
BMP5	Lys
BMP6	Lys

hOP-1	Leu	Asn	Ala	Ile	Ser	Val	Leu	Tyr	Phe
mOP-1
hOP-2	...	Ser	...	Thr	Tyr
mOP-2	...	Ser	...	Thr	Tyr
Vgl	Met	Ser	Pro	Met	...	Phe	Tyr
Vgr-1	Val
DPP	...	Asp	Ser	Val	Ala	Met	Leu
CBMP-2A	...	Ser	Met	Leu
CBMP-2B	...	Ser	Met	Leu
BMP3	Met	Ser	Ser	Leu	...	Ile	...	Phe	Tyr
GDF-1	...	Ser	Pro	Phe	...
60A	...	Gly	...	Leu	Pro	His
BMP5
BMP6
				75					80

hOP-1	Asp	Asp	Ser	Ser	Asn	Val	Ile	Leu	Lys
mOP-1
hOP-2	...	Ser	...	Asn	Arg
mOP-2	...	Ser	...	Asn	Arg
DPP	Asn	...	Gln	...	Thr	...	Val
Vgl	...	Asn	Asn	Asp	Val	...	Arg
Vgr-1	Asn
CBMP-2A	...	Glu	Asn	Glu	Lys	...	Val
CBMP-2B	...	Glu	Tyr	Asp	Lys	...	Val
BMP3	...	Glu	Asn	Lys	Val
GDF-1	...	Asn	...	Asp	Val	...	Arg
60A	Leu	Asn	Asp	Glu	Asn
BMP5
BMP6	Asn

hOP-1	Lys	Tyr	Arg	Asn	Met	Val	Val	Arg
mOP-1
hOP-2	...	His	Lys
mOP-2	...	His	Lys
DPP	Asn	...	Gln	Glu	...	Thr	...	Val
Vgl	His	...	Glu	Ala	...	Asp
Vgr-1
CBMP-2A	Asn	...	Gln	Asp	Glu
CBMP-2B	Asn	...	Gln	Glu	Glu
BMP3	Val	...	Pro	Thr	...	Glu
GDF-1	Gln	...	Glu	Asp	Asp
60A	Ile	...	Lys
BMP5
BMP6	Trp
	90					95		

hOP-1	Ala	Cys	Gly	Cys	His
mOP-1
hOP-2
mOP-2
DPP	Gly	Arg
Vgl	Glu	Arg
Vgr-1
CBMP-2A	Gly	Arg
CBMP-2B	Gly	Arg
BMP3	Ser	...	Ala	...	Arg
GDF-1	Glu	Arg
60A	Ser
BMP5	Ser
BMP6

100

**Between residues 56 and 57 of BMP3 is a Val residue;
between residues 43 and 44 of GDF-1 lies
the amino acid sequence Gly-Gly-Pro-Pro.

As is apparent from the foregoing amino acid sequence comparisons, significant amino acid changes can be made within the generic sequences while retaining the morphogenic activity. For example, while the GDF-1 protein sequence depicted in Table II shares only about 50% amino acid identity with the hOP1 sequence described therein, the GDF-1 sequence shares greater than 70% amino acid sequence homology (or "similarity") with the hOP1 sequence, where "homology" or "similarity" includes allowed conservative amino acid changes within the sequence as defined by Dayoff, et al., Atlas of Protein Sequence and Structure vol.5, supp.3, pp.345-362, (M.O. Dayoff, ed., Nat'l BioMed. Res. Fd'n, Washington D.C. 1979.)

The currently most preferred protein sequences detectable as morphogens in this invention include those having greater than 60% identity, preferably greater than 65% identity, with the amino acid sequence defining the conserved six cysteine skeleton of hOP1 (e.g., residues 43-139 of Seq. ID No. 5). These most preferred sequences include both allelic and species variants of the OP-1 and OP-2 proteins, including the *Drosophila* 60A protein. Accordingly, in still another preferred aspect, the invention includes detection of morphogens comprising species of polypeptide chains having the generic amino acid sequence referred to herein as "OPX", which defines the seven cysteine skeleton and accommodates the identities between the various identified mouse and human OP1 and OP2 proteins. OPX is presented in Seq. ID No. 29. As described therein, each Xaa at a given position

independently is selected from the residues occurring at the corresponding position in the C-terminal sequence of mouse or human OP1 or OP2 (see Seq. ID Nos. 5-8 and/or Seq. ID Nos. 16-23).

3. Tissue-Specific Expression of OP-1

Once a morphogen is identified in a tissue, its level may be determined either at the protein or nucleic acid level. By comparing the levels of production of a given morphogen among different tissues, it is possible to determine the tissue(s) of origin of that morphogen. The level of production of the morphogen OP-1 in different tissues is one example of a morphogen having a tissue of origin, i.e., the kidney, which contains a cell type that can also be used as the cell type which is used to screen, according to the invention, different compounds for their potential effects on morphogen (OP-1) production.

The level of OP-1 varies among different tissue types. In order to screen compounds for their effect on the production of OP-1 by a given cell type, it may be desirable to determine which tissues produce levels of OP-1 which are sufficiently high to show a potential decrease and sufficiently low to show a potential increase in production. Different tissues may be screened at the RNA level as follows.

Any probe capable of hybridizing specifically to a transcript, and distinguishing the transcript of interest from other, related transcripts may be used. Because the morphogens to be detected in the methods of this invention share such high sequence homology in their C-terminal domain, the tissue distribution of a specific morphogen transcript may best be determined using a probe specific

for the "pro" region of the immature protein and/or the N-terminal heterogeneous region of the mature protein. Another useful probe sequence is the 3' non-coding region immediately following the stop codon. These portions of the sequence vary substantially among the morphogens of this invention, and accordingly, are specific for each protein. For example, a particularly useful Vgr-1-specific probe sequence is the PvuII-SacI fragment, a 265 bp fragment encoding both a portion of the pro region and the N-terminus of the mature sequence. Similarly, particularly useful mOP-1-specific probe sequences are the BstXI-BglI fragment, a 0.68kb sequence that covers approximately two-thirds of the mOP1 pro region; a StuI-StuI fragment, a 0.2 kb sequence immediately upstream of the 7-cysteine domain, and an EarI-PstI fragment, a 0.3kb fragment containing the 3'untranslated sequence. Similar approaches may be used, for example, with hOP-1 (SEQ. ID NO.16) or human or mouse OP-2 (SEQ. ID NOS.20 and 22).

Using morphogen-specific oligonucleotide probes, morphogen transcripts can be identified in mammalian tissues, using standard methodologies well known to those having ordinary skill in the art. Briefly, total RNA from mouse embryos and organs from post-natal animals is prepared using the acid guanidine thiocyanate-phenol-chloroform method (Chomczynski et al., Anal. Biochem. 162:156-159, 1987). The RNA may be dissolved in TES buffer (10 mM Tris-HCl, 1 mM EDTA, 0.1% SDS, pH 7.5) and treated with Proteinase K (approx. 1.5 mg per g tissue sample) at 45°C for 1 hr. Poly(A)⁺ RNA selection on oligo(dT)-cellulose (Type 7, Pharmacia LKB Biotechnology Inc., Piscataway, NJ) may be done in a batch procedure by mixing 0.1 g oligo(dT)-cellulose with 11 ml RNA solution (from 1 g

tissue) in TES buffer and 0.5 M NaCl). Thereafter the oligo(dT) cellulose is washed in binding buffer (0.5 M NaCl, 10 mM Tris-HCl, 1 mM EDTA, pH 7.5) and poly(A)⁺ RNA is eluted with water. Poly(A)⁺ RNA (5 or 15 µg/lane) is fractionated on 1 or 1.2% agarose-formaldehyde gels (Selden, in Current Protocols in Molecular Biology, Ausubel et al. eds., pp. 1-4, 8, 9, Greene Publishing and Wiley-Interscience, New York, 1991). 1 µl of 400 µg/ml ethidium bromide is added to each sample prior to heat denaturation (Rosen et al., Focus 12:23-24, 1990). Following electrophoresis, the gels are photographed and the RNA is blotted overnight onto Nytran nitrocellulose membranes (Schleicher & Schuell Inc., Keene, NH) with 10 x SSC. The membranes are baked at 80°C for 30-60 min. and irradiated with UV light (1 mW/cm² for 25 sec.). The Northern hybridization conditions may be as previously described (Ozkaynak et al., EMBO J. 9:2085-2093, 1990). For re-use, the filters may be deprobed in 1 mM Tris-HCl, 1 mM EDTA, 0.1% SDS, pH 7.5, at 90-95°C and exposed to film to assure complete removal of previous hybridization signals.

One probe which may be used to screen for transcripts encoding a morphogen includes a portion of or the complete OP-1 cDNA, which may be used to detect the presence of OP-1 mRNA or mRNAs of related morphogens. The sequence of the murine cDNA gene is set forth in SEQ ID NO:14.

OP-1 mRNA expression was analyzed in 17 day mouse embryos and 3 day post-natal mice by sequentially hybridizing filters with various probes. Probes from regions other than the highly conserved 7-cysteine domain were selected because this region is highly variable among

members of the TGF- β superfamily. Fig. 1 shows the fragments of OP-1, used as probes in the Northern hybridizations. The solid box indicates the putative signal peptide and the hatched box corresponds to the TGF- β -like domain that contains the seven cysteine residues. Asterisks indicate the potential N-glycosylation sites. The arrow marks the location of the cleavage site for OP-1 maturation. Three solid bars below the diagram indicate the OP-1 specific fragments used in making 32 P-labeled probes (0.68 kb BstXI - BglI fragment, 0.20 kb StuI - StuI fragment and 0.34 kb EarI - PstI non-coding fragment).

Hybridization with a probe that covers approximately two thirds of the pro region (the 0.68 kb BstXI-BglI fragment), reveals a 4 kb message and 3 messages at 1.8 kb, 2.2 kb and 2.4 kb (Fig. 2B and D, and Fig. 3). In the Northern hybridization of Fig. 2, equal amounts (15 μ g) of poly(A)⁺ RNA were loaded into each lane, electrophoresed on a 1% agarose-formaldehyde gel, blotted and hybridized. A 0.24 - 9.49 kb RNA ladder (Bethesda Research Labs, Inc.) was used as size standard. The same filter was used for sequential hybridizations with labeled probes specific for OP-1 (Panels B and D), Vgr-1 (Panel C), and EF-Tu (Panel A). Panel A: the EF-Tu specific probe (a control) was the 0.4 kb HindIII-SacI fragment (part of the coding region), the SacI site used belonged to the vector; Panel B: the OP-1 specific probe was the 0.68 kb BstXI-BglI fragment (two thirds of the pro region and upstream sequences of the mature domain, not including any sequences from the 7-cysteine domain); Panel C: the Vgr-1 specific probe was the 0.26 kb PvuII-SacI fragment (part of the pro region and the amino-terminal sequences of the mature

domain, including the first cysteine) (Lyons et al., 1989, Proc. Nat. Aca. Sci. 86: 4554, hereby incorporated by reference). Panel D: the OP-1 (3' flanking) specific probe was the 0.34 kb *EarI*-*PstI* fragment (3' untranslated sequences immediately following the sequences encoding OP-1).

In Fig. 3, the tissues to be used for RNA preparation were obtained from two week old mice (Panel A) or 5 week old mice (Panel B), with the exception of poly A+ RNA which was obtained from kidney adrenal gland of two week old mice (Panel B). Equal amounts of poly A+ RNA (15 μ g for Panel A and 5 μ g for Panel B) were loaded into each well. After electrophoresis (1.2% agarose-formaldehyde gels) and blotting, RNA was hybridized to the OP-1 specific 3' flanking probe described in the legend of Fig. 2 (Panel D). The 0.24-9.5 kb RNA ladder was used as size standard. The arrowheads indicate the OP-1 specific messages. The lower section of Panels A and B show the hybridization pattern obtained with the EF-Tu specific probe (a control).

Although the size of the Vgr-1 specific message is close to the 4 kb OP-1 species (Fig. 2 Panel C), the OP-1 4 kb mRNA is somewhat larger. To further rule out cross-hybridization with a non-OP-1 message, the 0.2 kb *StuI*-*StuI* fragment which represents the gene specific sequences immediately upstream of those encoding the 7-cysteine domain was used. This probe gave a hybridization pattern similar to the one shown in Fig. 2 Panel B (data not shown). A third probe, the 0.34 kb *EarI*-*PstI* fragment containing 3' untranslated sequences, also confirmed the pattern (Fig. 2 Panel D). Thus, the same four OP-1 specific messages were observed with three distinct probes.

The appearance of a new 4 kb OP-1 mRNA species was initially interpreted as cross hybridization of the OP-1 probe with Vgr-1 mRNA, which is approximately this size (Fig. 2 Panel C). However, the 4 kb message was detected with three different OP-1 specific probes, including one specific to the 3' untranslated region, and moreover it was separated from Vgr-1 message on the basis of size. Most likely, therefore, the 4 kb mRNA (and the three species of 1.8 kb, 2.2 kb and 2.4 kb) results from alternative splicing of OP-1 transcripts. The 4 kb OP-1 mRNA could also represent a bicistronic mRNA. The 4 kb message is a minor species in kidney, while it is more prominent in adrenal tissue.

The level of OP-1 expression was compared in different tissues using poly(A)⁺ RNA prepared from brain, spleen, lung, kidney and adrenal gland, heart, and liver of 13 day post-natal mice. The RNA was analyzed on Northern blots by hybridization to various probes (Fig. 3. Equal amounts of mRNA, as judged by optical density, were fractionated on agarose formaldehyde gels. Ethidium bromide staining of the gels revealed some residual ribosomal RNA in addition to the mRNA and provided another assurance that the mRNA was not degraded and that there was not significant quantitative or qualitative variation in the preparation. As control for mRNA recovery, EF-Tu (translational elongation factor) mRNA was probed (assuming uniform expression of EF-Tu in most tissues). A great variation in the level of OP-1 expression was observed in spleen, lung, kidney and adrenal tissues whereas EF-Tu mRNA levels appeared relatively constant in these tissues (Fig. 3 Panel A). The highest level of OP-1 mRNA was found in the kidneys. Uniformly lower levels of EF-Tu mRNA were

found in brain, heart and liver (Fig. 3 Panel A). Additional analysis of OP-1 mRNA showed the presence of significant amounts of OP-1 mRNA in the bladder (data not shown). In summary, next to kidney, bladder and adrenal tissue, brain tissue contained the highest levels of OP-1 RNA, whereas heart and liver did not give detectable signals.

OP-1 mRNA patterns display qualitative changes in the various tissues. Of the four messages found in brain, the 2.2 kb message is most abundant whereas in lung and spleen the 1.8 kb message predominates. Levels of the 1.8-2.4 kb in the kidney OP-1 mRNA are approximately two times higher in 3 day post-natal mice than in 17 day embryos, perhaps reflecting phases in bone and/or kidney development. mRNA was also prepared from carefully separated renal and adrenal tissues of 5 week old mice. Northern blot analysis (Figure 4, Panel B) revealed that the high levels of 2.2 kb mRNA were derived from renal tissue whereas the 4 kb mRNA was more prominent in adrenal tissue.

The detection of of OP-1 message primarily in the kidney but also in bladder links OP-1 expression specifically with the urinary tract. Interestingly, the related Vgr-1 is also expressed at significant levels in kidney although its main site of expression in lung.

Once the tissue-specific expression of a given morphogen is known, cell types known to exist in that tissue or cell lines derived from that tissue can be screened, in a similar manner, to identify the cell type within that tissue that is actually responsible for the tissue specific synthesis and secretion of the morphogen. Once a cell type which produces the morphogen in an amount

sufficient to detect increases or decreases in the production level of the morphogen upon exposure to a compound is identified, it may be used in tissue culture assay to rapidly screen for the ability of compound to upregulate or down regulate the synthesis and secretion of the morphogen. The level of morphogen production by the chosen cell type is determined with and without incubating the cell in culture with the compound, in order to assess the effects of the compound on the cell's ability to synthesize or secrete the morphogen. This can be accomplished by detection of the level of production of the morphogen either at the protein or mRNA level.

4. Growth of Cells in Culture

Cell cultures derived from kidney, adrenals, urinary bladder, brain, or other organs, may be prepared as described widely in the literature. For example, kidneys may be explanted from neonatal, new born, young or adult rodents (mouse or rat) and used in organ culture as whole or sliced (1-4 mm) tissues. Primary tissue cultures and established cell lines, also derived from kidney, adrenals, urinary, bladder, brain, or other tissues may be established in multiwell plates (6 well, 24 well, or 96 well) according to conventional cell culture techniques, and are cultured in the absence or presence of serum for a period of time (1-7 days). Cells may be cultured, for example, in Dulbecco's Modified Eagle medium (Gibco, Long Island, NY) containing serum (e.g., fetal calf serum at 1%-10%, Gibco) or in serum-deprived medium, as desired, or in defined medium (e.g., containing insulin, transferrin, glucose, albumin, or other growth factors).

Samples for testing the level of morphogen production include culture supernatants or cell lysates, collected periodically and evaluated for OP-1 production by immunoblot analysis of a portion of the cell culture itself, collected periodically and used to prepare polyA+ RNA for RNA analysis (Sambrook et al., eds., Molecular Cloning, 1989, Cold Spring Harbor Press, Cold Spring Harbor, NY). To monitor de novo OP-1 synthesis, some cultures are labeled with ^{35}S -methionine/ ^{35}S -cysteine mixture for 6-24 hours and then evaluated for morphogen production by conventional immunoprecipitation methods (Sambrook et al., eds., Molecular Cloning, 1989, Cold Spring Harbor Press, Cold Spring Harbor, NY). Alternatively, the production of morphogen or determination of the level of morphogen production may be ascertained using a simple assay for a parameter of cell growth, e.g., cellular proliferation or death. For example, where a morphogen is produced by a cultured cell line, the addition of antibody specific for the morphogen may result in relief from morphogen inhibition of cell growth. Thus, measurement of cellular proliferation can be used as an indication of morphogen production by a tissue.

5. Determination of Level of Morphogenic Protein

In order to quantitate the production of a morphogenic protein by a cell type, an immunoassay may be performed to detect the morphogen using a polyclonal or monoclonal antibody specific for that morphogen. For example, OP-1 may be detected using a polyclonal antibody specific for OP-1 in an ELISA, as follows.

1 μg /100 μl of affinity-purified polyclonal rabbit IgG specific for OP-1 is added to each well of a 96-well

plate and incubated at 37°C for an hour. The wells are washed four times with 0.16M sodium borate buffer with 0.15 M NaCl (BSB), pH 8.2, containing 0.1% Tween 20. To minimize non-specific binding, the wells are blocked by filling completely with 1% bovine serum albumin (BSA) in BSB for 1 hour at 37°C. The wells are then washed four times with BSB containing 0.1% Tween 20. A 100 ul aliquot of an appropriate dilution of each of the test samples of cell culture supernatant is added to each well in triplicate and incubated at 37°C for 30 min. After incubation, 100 ul biotinylated rabbit anti-OP-1 serum (stock solution is about 1 mg/ml and diluted 1:400 in BSB containing 1% BSA before use) is added to each well and incubated at 37°C for 30 min. The wells are then washed four times with BSB containing 0.1% Tween 20. 100 ul streptavidin-alkaline (Southern Biotechnology Associates, Inc. Birmingham, Alabama, diluted 1:2000 in BSB containing 0.1% Tween 20 before use) is added to each well and incubated at 37°C for 30 min. The plates are washed four times with 0.5M Tris buffered Saline (TBS), pH 7.2. 50ul substrate (ELISA Amplification System Kit, Life Technologies, Inc., Bethesda, MD) are added to each well incubated at room temperature for 15 min. Then, 50 ul amplifier (from the same amplification system kit) is added and incubated for another 15 min at room temperature. The reaction is stopped by the addition of 50 ul 0.3 M sulphuric acid. The OD at 490 nm of the solution in each well is recorded. To quantitate OP-1 in culture media, a OP-1 standard curve is performed in parallel with the test samples.

6. Preparation of Polyclonal Antibody

Polyclonal antibody is prepared as follows. Each rabbit is given a primary immunization of 100 ug/500 ul E. coli-produced OP-1 monomer (amino acids 328-431 of SEQ. ID NO: 11) in 0.1% SDS mixed with 500 ul Complete Freund's Adjuvant. The antigen is injected subcutaneously at multiple sites on the back and flanks of the animal. The rabbit is boosted after a month in the same manner using incomplete Freund's Adjuvant. Test bleeds are taken from the ear vein seven days later. Two additional boosts and test bleeds are performed at monthly intervals until antibody against OP-1 is detected in the serum using an ELISA assay. Then, the rabbit is boosted monthly with 100 ug of antigen and bled (15 ml per bleed) at days seven and ten after boosting.

7. Preparation of Monoclonal Antibody and Neutralizing Monoclonal Antibody

Monoclonal antibody specific for a given morphogen may be prepared as follows. A mouse is given two injections of E. coli produced OP-1 monomer (amino acids 328-431 in SEQ ID NO:11). The first injection contains 100ug of OP-1 in complete Freund's adjuvant and is given subcutaneously. The second injection contains 50 ug of OP-1 in incomplete adjuvant and is given intraperitoneally. The mouse then receives a total of 230 ug of OP-1 (amino acids 307-431 of SEQ ID NO:11) in four intraperitoneal injections at various times over an eight month period. One week prior to fusion, The mouse is boosted intraperitoneally with 100 ug of OP-1 (15-139) and 30 ug of the N-terminal peptide (Ser293-Asn309-Cys) conjugated through the added cys residue to bovine serum albumin with

SMCC crosslinking agent. This boost is repeated five days (IP), four days (IP), three days (IP) and one day (IV) prior to fusion. The mouse spleen cells are then fused to myeloma (e.g., 653) cells at a ratio of 1:1 using PEG 1500 (Boehringer Mannheim), and the cell fusion is plated and screened for OP-1-specific antibodies using OP-1 (307-431) as antigen. The cell fusion and monoclonal screening are according to procedures widely available in the art. The neutralizing monoclonal is identified by its ability to block the biological activity of OP-1 when added to a cellular assay which responds biologically to added OP-1.

8. Identification of OP-1 Producing Cell Line Which Displays OP-1 Surface Receptors

During the process of routinely testing the effects of increasing concentrations of OP-1 and TGF- β on the proliferation of various cell lines, a cell line was identified which, surprising, appears not only to synthesize and secrete OP-1, but also to display cell surface receptors to which the secreted OP-1 binds and acts to inhibit proliferation of the cells. This cell line was identified after the following observations. Addition of increasing concentrations of OP-1 or TGF- β failed to increase or decrease the relatively low basal rate of proliferation of the cells. However, addition of a monoclonal antibody, which neutralizes the activity of OP-1, resulted in a large increase in the proliferation of the cells. In addition, simultaneous addition of the same quantity of OP-1 neutralizing monoclonal to a fixed amount of OP-1 resulted in an increase in proliferation which was intermediate between the low

basal level observed with OP-1 alone and the high level observed with the monoclonal alone. This cell line, which is an epithelial cell line that was derived from a bladder cell carcinoma, may be used in an assay of the invention. The parameter to be tested according to the invention is cellular proliferation. Thus, a compound(s) that increases or decreases the level of OP-1 production may be tested on this cell line as follows..

9. Assay for Identifying Drugs Which Affect OP-1 Synthesis

A simple medium flux screening assay can be configured in a standard 24 or 96 well microtiter dish, in which each well contains a constant number of a cell line having the characteristics described above. Increasing concentrations of an OP-1 neutralizing monoclonal antibody is added from left to right across the dish. A constant amount of different test substances is added from top to bottom on the dish. An increase in the synthesis and secretion of OP-1 (over its constitutive (non-induced) level) will be indicated by an increase in the amount of OP-1 neutralizing antibody required to release the cells from the antimitogenic activity of OP-1. A decrease in the synthesis and secretion of OP-1 (below its constitutive (repressed) level) will be indicated by the observation that decreased concentrations of the OP-1 neutralizing monoclonal antibody will be required to release the cells from the antimitogenic activity of OP-1. One of the major advantages of this assay is that the end point, i.e., the dilution of antibody which has an effect on cell proliferation, is a measure of mitosis, or an increase in

the number of cells per well. Because several convenient and rapid assays exist for quantitating cell numbers, this assay is faster and requires significantly fewer steps to perform.

The assay may be performed as follows. After addition of appropriate concentrations of the OP-1 neutralizing monoclonal antibody and test substances to the wells containing the cells, the dishes are placed in an incubator at 37°C for a period of 1-3 days. After completion of incubation/growth period, the dishes are removed and the cells in the individual wells are washed and stained with a vital stain, such as crystal violet. Washing and staining procedures are well-known in the art. The cells are then lysed and the stain dissolved in a constant amount of a solvent, such as ethanol. Quantitations of the dissolved stain, which is readily performed on an automated plate vendor, allows for direct quantitation of the number of cells in each well.

The above-described assay has the advantages of being rapid and easy to perform because it requires few steps. Another advantage is intrinsic to the assay; drugs which are screened according to this procedure that result in cell death (i.e., cytotoxic substances) are immediately, identifiable without the need of operator observation. In addition, although drugs that stop the growth of the cells (i.e., cytostatic substances) are scored as positive due to failure to see increases in cell numbers, they are automatically scored as suspect due to the failure of the highest concentrations of OP-1 neutralizing monoclonal antibody to release the cells from the antimitogenic activity of OP-1.

10. Candidate Drugs to Screen

The screening methods of the invention is used to test compounds for their effect on the production of morphogenic protein by a given cell type. Examples of compounds which may be screened include but are not limited to chemicals, biological response modifiers (e.g., lymphokines, cytokines, hormones, or vitamins), plant extracts, microbial broths and extracts medium conditioned by eukaryotic cells, body fluids, or tissue extracts.

The invention may be embodied in other specific forms without departing from the spirit or essential characteristics thereof. The present embodiments are therefore to be considered in all respects as illustrative and not restrictive, the scope of the invention being indicated by the appended claims rather than by the foregoing description, and all changes which come within the meaning and range of equivalency of the claims are therefore intended to be embraced therein.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: John Smart
Herman Oppermann
Engin Ozkaynak
Thangavel Kuberasampath
David C. Rueger
Roy H.L. Pang
Charles M. Cohen
- (ii) TITLE OF INVENTION: MORPHOGENIC
PROTEIN SCREENING METHOD
- (iii) NUMBER OF SEQUENCES: 33
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Creative BioMolecules
 - (B) STREET: 35 South Street
 - (C) CITY: Hopkinton
 - (D) STATE: Massachusetts
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 01748
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette, 5.25,
360kb storage
 - (B) COMPUTER: IBM XT
 - (C) OPERATING SYSTEM: DOS 3.30
 - (D) SOFTWARE: ASC II TEXT
- (vi) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 667,274
 - (B) FILING DATE: March 11, 1991
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 752,861
 - (B) FILING DATE: AUGUST 30, 1991

(viii) ATTORNEY/AGENT INFORMATION

(A) NAME: PITCHER, EDMUND R.

(B) REG. NO.: 27,829

(C) DOCKET NO.: CRP-058PC

(ix) TELEPHONE:

(A) 617/248-7000

(B) TELEFAX: 617/248-7100

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acids

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME: Generic Sequence 1

(D) OTHER INFORMATION: Each Xaa indicates one of the 20 naturally-occurring L-isomer, α -amino acids or a derivative thereof.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```

Xaa Xaa Xaa Xaa Xaa Xaa
      1               5
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
      10             15
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa
      20             25
Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
      30             35
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
      40             45             50
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
      55             60
Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
      65             70
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
      75             80
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
      85             90
Xaa Cys Xaa
      95

```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acids

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME: Generic Sequence 2

(D) OTHER INFORMATION: Each Xaa indicates one of the 20 naturally-occurring L-isomer, α -amino acids or a derivative thereof.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa					
	1						5				
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			10					15			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	
			20				25				
Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	
			30				35				
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
40						45					50
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys
					55					60	
Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
					65					70	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
					75					80	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys
					85					90	
Xaa	Cys	Xaa									
											95

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acids

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME: Generic Sequence 3

(D) OTHER INFORMATION: wherein each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

      Leu Tyr Val Xaa Phe
      1               5
Xaa Xaa Xaa Gly Trp Xaa Xaa Trp Xaa
      10
Xaa Ala Pro Gly Xaa Xaa Xaa Ala
      15               20
Xaa Tyr Cys Xaa Gly Xaa Cys Xaa
      25               30
Xaa Pro Xaa Xaa Xaa Xaa Xaa
      35
Xaa Xaa Xaa Asn His Ala Xaa Xaa
      40               45
Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa
      50
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
      55               60
Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa
      65

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Xaa Xaa Xaa Leu Xaa Xaa Xaa
 70                               75
Xaa Xaa Xaa Xaa Val Xaa Leu Xaa
                        80
Xaa Xaa Xaa Xaa Met Xaa Val Xaa
 85                               90
Xaa Cys Gly Cys Xaa
                        95

```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acids

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME: Generic Sequence 4

(D) OTHER INFORMATION: wherein each
Xaa is independently selected from
a group of one or more specified
amino acids as defined in the
specification.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Cys Xaa Xaa Xaa Xaa Leu Tyr Val Xaa Phe
 1                               5                               10
Xaa Xaa Xaa Gly Trp Xaa Xaa Trp Xaa
                        15
Xaa Ala Pro Xaa Gly Xaa Xaa Ala
 20                               25
Xaa Tyr Cys Xaa Gly Xaa Cys Xaa
      30                               35
Xaa Pro Xaa Xaa Xaa Xaa Xaa
                        40

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Asn Xaa Xaa Asn His Ala Xaa Xaa
      45                      50
Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa
      55
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
      60                      65
Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa
      70
Xaa Xaa Xaa Leu Xaa Xaa Xaa
      75                      80
Xaa Xaa Xaa Xaa Val Xaa Leu Xaa
      85
Xaa Xaa Xaa Xaa Met Xaa Val Xaa
      90                      95
Xaa Cys Gly Cys Xaa
      100

```

- (2) INFORMATION FOR SEQ ID NO:5:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 139 amino acids
 - (B) TYPE: amino acids
 - (C) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (ix) FEATURE:
 - (A) NAME: hOP-1 (mature form)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

Ser  Thr  Gly  Ser  Lys  Gln  Arg  Ser  Gln
 1                      5
Asn  Arg  Ser  Lys  Thr  Pro  Lys  Asn  Gln
10                      15
Glu  Ala  Leu  Arg  Met  Ala  Asn  Val  Ala
      20                      25
Glu  Asn  Ser  Ser  Ser  Asp  Gln  Arg  Gln
      30                      35

```

Ala	Cys	Lys	Lys	His	Glu	Leu	Tyr	Val
			40					45
Ser	Phe	Arg	Asp	Leu	Gly	Trp	Gln	Asp
			50					
Trp	Ile	Ile	Ala	Pro	Glu	Gly	Tyr	Ala
55					60			
Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ala
	65					70		
Phe	Pro	Leu	Asn	Ser	Tyr	Met	Asn	Ala
		75					80	
Thr	Asn	His	Ala	Ile	Val	Gln	Thr	Leu
			85					90
Val	His	Phe	Ile	Asn	Pro	Glu	Thr	Val
			95					
Pro	Lys	Pro	Cys	Cys	Ala	Pro	Thr	Gln
100					105			
Leu	Asn	Ala	Ile	Ser	Val	Leu	Tyr	Phe
	110					115		
Asp	Asp	Ser	Ser	Asn	Val	Ile	Leu	Lys
		120					125	
Lys	Tyr	Arg	Asn	Met	Val	Val	Arg	Ala
			130					135
Cys	Gly	Cys	His					

- (2) INFORMATION FOR SEQ ID NO:6:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 139 amino acids
 - (B) TYPE: amino acids
 - (C) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (ix) FEATURE:
 - (A) NAME: mOP-1 (mature form)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ser	Thr	Gly	Gly	Lys	Gln	Arg	Ser	Gln
1				5				
Asn	Arg	Ser	Lys	Thr	Pro	Lys	Asn	Gln
10					15			
Glu	Ala	Leu	Arg	Met	Ala	Ser	Val	Ala
	20					25		
Glu	Asn	Ser	Ser	Ser	Asp	Gln	Arg	Gln
		30					35	
Ala	Cys	Lys	Lys	His	Glu	Leu	Tyr	Val
			40					45
Ser	Phe	Arg	Asp	Leu	Gly	Trp	Gln	Asp
				50				
Trp	Ile	Ile	Ala	Pro	Glu	Gly	Tyr	Ala
55					60			
Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ala
	65					70		
Phe	Pro	Leu	Asn	Ser	Tyr	Met	Asn	Ala
		75					80	
Thr	Asn	His	Ala	Ile	Val	Gln	Thr	Leu
			85					90
Val	His	Phe	Ile	Asn	Pro	Asp	Thr	Val
				95				
Pro	Lys	Pro	Cys	Cys	Ala	Pro	Thr	Gln
100					105			
Leu	Asn	Ala	Ile	Ser	Val	Leu	Tyr	Phe
	110					115		

Asp	Asp	Ser	Ser	Asn	Val	Ile	Leu	Lys
		120					125	
Lys	Tyr	Arg	Asn	Met	Val	Val	Arg	Ala
			130					135
Cys	Gly	Cys	His					

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acids

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME: hOP-2 (mature form)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ala	Val	Arg	Pro	Leu	Arg	Arg	Arg	Gln
1				5				
Pro	Lys	Lys	Ser	Asn	Glu	Leu	Pro	Gln
10					15			
Ala	Asn	Arg	Leu	Pro	Gly	Ile	Phe	Asp
20						25		
Asp	Val	His	Gly	Ser	His	Gly	Arg	Gln
		30					35	
Val	Cys	Arg	Arg	His	Glu	Leu	Tyr	Val
			40					45
Ser	Phe	Gln	Asp	Leu	Gly	Trp	Leu	Asp
				50				
Trp	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser
55					60			
Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ser
65						70		
Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	Ala
		75					80	
Thr	Asn	His	Ala	Ile	Leu	Gln	Ser	Leu
			85					90

Val	His	Leu	Met	Lys	Pro	Asn	Ala	Val
				95				
Pro	Lys	Ala	Cys	Cys	Ala	Pro	Thr	Lys
100					105			
Leu	Ser	Ala	Thr	Ser	Val	Leu	Tyr	Tyr
	110					115		
Asp	Ser	Ser	Asn	Asn	Val	Ile	Leu	Arg
		120					125	
Lys	His	Arg	Asn	Met	Val	Val	Lys	Ala
			130					135
Cys	Gly	Cys	His					

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acids

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME: mOP-2 (mature form)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ala	Ala	Arg	Pro	Leu	Lys	Arg	Arg	Gln
1				5				
Pro	Lys	Lys	Thr	Asn	Glu	Leu	Pro	His
10					15			
Pro	Asn	Lys	Leu	Pro	Gly	Ile	Phe	Asp
	20					25		
Asp	Gly	His	Gly	Ser	Arg	Gly	Arg	Glu
		30					35	
Val	Cys	Arg	Arg	His	Glu	Leu	Tyr	Val
			40					45
Ser	Phe	Arg	Asp	Leu	Gly	Trp	Leu	Asp
				50				
Trp	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser
55					60			

Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ala
	65					70		
Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	Ala
		75					80	
Thr	Asn	His	Ala	Ile	Leu	Gln	Ser	Leu
			85					90
Val	His	Leu	Met	Lys	Pro	Asp	Val	Val
				95				
Pro	Lys	Ala	Cys	Cys	Ala	Pro	Thr	Lys
100					105			
Leu	Ser	Ala	Thr	Ser	Val	Leu	Tyr	Tyr
	110					115		
Asp	Ser	Ser	Asn	Asn	Val	Ile	Leu	Arg
		120					125	
Lys	His	Arg	Asn	Met	Val	Val	Lys	Ala
			130					135
Cys	Gly	Cys	His					

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acids

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) **FEATURE:**

(A) NAME: CBMP-2A(fx)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

[illegible]

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 amino acids

(B) TYPE: amino acids

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) **FEATURE:**

(A) NAME: CBMP-2B(fx)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

						Cys	Arg	Arg	His	Ser	
						1				5	
Leu	Tyr	Val	Asp	Phe	Ser	Asp	Val	Gly	Trp	Asn	
				10						15	
Asp	Trp	Ile	Val	Ala	Pro	Pro	Gly	Tyr	Gln	Ala	
			20						25		
Phe	Tyr	Cys	His	Gly	Asp	Cys	Pro	Phe	Pro	Leu	
		30					35				
Ala	Asp	His	Leu	Asn	Ser	Thr	Asn	His	Ala	Ile	
	40					45					
Val	Gln	Thr	Leu	Val	Asn	Ser	Val	Asn	Ser	Ser	
50					55					60	
Ile	Pro	Lys	Ala	Cys	Cys	Val	Pro	Thr	Glu	Leu	
			65							70	
Ser	Ala	Ile	Ser	Met	Leu	Tyr	Leu	Asp	Glu	Tyr	
			75						80		
Asp	Lys	Val	Val	Leu	Lys	Asn	Tyr	Gln	Glu	Met	
	85						90				
Val	Val	Glu	Gly	Cys	Gly	Cys	Arg				
	95					100					

- (2) INFORMATION FOR SEQ ID NO:11:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acids
 - (C) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (ix) FEATURE:
 - (A) NAME: DPP(fx)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Cys	Arg	Arg	His	Ser	Leu	Tyr	Val	Asp	Phe	Ser										
1				5					10											
Asp	Val	Gly	Trp	Asp	Asp	Trp	Ile	Val	Ala	Pro										
			15						20											
Leu	Gly	Tyr	Asp	Ala	Tyr	Tyr	Cys	His	Gly	Lys										
			25					30												
Cys	Pro	Phe	Pro	Leu	Ala	Asp	His	Phe	Asn	Ser										
			35				40													
Thr	Asn	His	Ala	Val	Val	Gln	Thr	Leu	Val	Asn										
			45				50			55										
Asn	Asn	Asn	Pro	Gly	Lys	Val	Pro	Lys	Ala	Cys										
				60					65											
Cys	Val	Pro	Thr	Gln	Leu	Asp	Ser	Val	Ala	Met										
			70					75												
Leu	Tyr	Leu	Asn	Asp	Gln	Ser	Thr	Val	Val	Leu										
			80				85													
Lys	Asn	Tyr	Gln	Glu	Met	Thr	Val	Val	Gly	Cys										
			90				95													
Gly	Cys	Arg																		
100																				

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(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acids

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME: Vgl(fx)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Cys	Lys	Lys	Arg	His	Leu	Tyr	Val	Glu	Phe	Lys		
1					5					10		
Asp	Val	Gly	Trp	Gln	Asn	Trp	Val	Ile	Ala	Pro		
			15						20			
Gln	Gly	Tyr	Met	Ala	Asn	Tyr	Cys	Tyr	Gly	Glu		
		25					30					
Cys	Pro	Tyr	Pro	Leu	Thr	Glu	Ile	Leu	Asn	Gly		
		35				40						
Ser	Asn	His	Ala	Ile	Leu	Gln	Thr	Leu	Val	His		
	45				50					55		
Ser	Ile	Glu	Pro	Glu	Asp	Ile	Pro	Leu	Pro	Cys		
				60					65			
Cys	Val	Pro	Thr	Lys	Met	Ser	Pro	Ile	Ser	Met		
			70					75				
Leu	Phe	Tyr	Asp	Asn	Asn	Asp	Asn	Val	Val	Leu		
		80					85					
Arg	His	Tyr	Glu	Asn	Met	Ala	Val	Asp	Glu	Cys		
		90				95						
Gly	Cys	Arg										
100												

- (2) INFORMATION FOR SEQ ID NO:13:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acids
 - (C) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (ix) FEATURE:
 - (A) NAME: Vgr-1(fx)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```

Cys Lys Lys His Glu Leu Tyr Val Ser Phe Gln
 1             5             10
Asp Val Gly Trp Gln Asp Trp Ile Ile Ala Pro
          15             20
Xaa Gly Tyr Ala Ala Asn Tyr Cys Asp Gly Glu
          25             30
Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala
          35             40
Thr Asn His Ala Ile Val Gln Thr Leu Val His
          45             50             55
Val Met Asn Pro Glu Tyr Val Pro Lys Pro Cys
          60             65
Cys Ala Pro Thr Lys Val Asn Ala Ile Ser Val
          70             75
Leu Tyr Phe Asp Asp Asn Ser Asn Val Ile Leu
          80             85
Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys
          90             95
Gly Cys His
100

```

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 106 amino acids
- (B) TYPE: protein
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human
- (F) TISSUE TYPE: BRAIN

(ix) FEATURE:

- (D) OTHER INFORMATION:
- /product= "GDF-1 (fx)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Cys	Arg	Ala	Arg	Arg	Leu	Tyr	Val	Ser	Phe	Arg	Glu	Val	Gly	
1				5					10					
Trp	His	Arg	Trp	Val	Ile	Ala	Pro	Arg	Gly	Phe	Leu	Ala	Asn	Tyr
15				20					25					
Cys	Gln	Gly	Gln	Cys	Ala	Leu	Pro	Val	Ala	Leu	Ser	Gly	Ser	Gly
30				35					40					
Gly	Pro	Pro	Ala	Leu	Asn	His	Ala	Val	Leu	Arg	Ala	Leu	Met	His
45				50					55					
Ala	Ala	Ala	Pro	Gly	Ala	Ala	Asp	Leu	Pro	Cys	Cys	Val	Pro	Ala
60				65					70					
Arg	Leu	Ser	Pro	Ile	Ser	Val	Leu	Phe	Phe	Asp	Asn	Ser	Asp	Asn
75				80					85					
Val	Val	Leu	Arg	Gln	Tyr	Glu	Asp	Met	Val	Val	Asp	Glu	Cys	Gly
90				95					100					
Cys	Arg													
105														

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Cys Xaa Xaa Xaa Xaa
 1 5

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1822 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: HOMO SAPIENS
 (F) TISSUE TYPE: HIPPOCAMPUS

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 49..1341
 (D) OTHER INFORMATION: /standard_name= "hOP1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGT GCG GGC CGG AGC CCG GGT A GCG GTAGAG CCG GCG ATG CAC GTG	57
Met His Val	
1	
CGC TCA CTG CGA GCT GCG GCG CCG CAC AGC TTC GTG GCG CTC TGG GCA	105
Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala	
5 10 15	
CCC CTG TTC CTG CTG CGC TCC GCC CTG GCC GAC TTC AGC CTG GAC AAC	153
Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn	
20 25 30 35	
GAG GTG CAC TCG AGC TTC ATC CAC CGG CGC CTC CGC AGC CAG GAG CGG	201
Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg	
40 45 50	
CGG GAG ATG CAG CGC GAG ATC CTC TCC ATT TTG GGC TTG CCC CAC CGC	249
Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg	
55 60 65	

CCG	CGC	CCG	CAC	CTC	CAG	GGC	AAG	CAC	AAC	TCG	GCA	CCC	ATG	TTC	ATG	297
Pro	Arg	Pro	His	Leu	Gln	Gly	Lys	His	Asn	Ser	Ala	Pro	Met	Phe	Met	
		70					75					80				
CTG	GAC	CTG	TAC	AAC	GCC	ATG	GCG	GTG	GAG	GAG	GGC	GGC	GGG	CCC	GGC	345
Leu	Asp	Leu	Tyr	Asn	Ala	Met	Ala	Val	Glu	Glu	Gly	Gly	Gly	Pro	Gly	
	85					90					95					
GGC	CAG	GGC	TTC	TCC	TAC	CCC	TAC	AAG	GCC	GTC	TTC	AGT	ACC	CAG	GGC	393
Gly	Gln	Gly	Phe	Ser	Tyr	Pro	Tyr	Lys	Ala	Val	Phe	Ser	Thr	Gln	Gly	
100					105					110					115	
CCC	CCT	CTG	GCC	AGC	CTG	CAA	GAT	AGC	CAT	TTC	CTC	ACC	GAC	GCC	GAC	441
Pro	Pro	Leu	Ala	Ser	Leu	Gln	Asp	Ser	His	Phe	Leu	Thr	Asp	Ala	Asp	
				120					125					130		
ATG	GTC	ATG	AGC	TTC	GTC	AAC	CTC	GTG	GAA	CAT	GAC	AAG	GAA	TTC	TTC	489
Met	Val	Met	Ser	Phe	Val	Asn	Leu	Val	Glu	His	Asp	Lys	Glu	Phe	Phe	
		135					140						145			
CAC	CCA	CGC	TAC	CAC	CAT	CGA	GAG	TTC	CGG	TTT	GAT	CTT	TCC	AAG	ATC	537
His	Pro	Arg	Tyr	His	His	Arg	Glu	Phe	Arg	Phe	Asp	Leu	Ser	Lys	Ile	
		150					155					160				
CCA	GAA	GGG	GAA	GCT	GTC	ACG	GCA	GCC	GAA	TTC	CGG	ATC	TAC	AAG	GAC	585
Pro	Glu	Gly	Glu	Ala	Val	Thr	Ala	Ala	Glu	Phe	Arg	Ile	Tyr	Lys	Asp	
	165					170					175					
TAC	ATC	CGG	GAA	CGC	TTC	GAC	AAT	GAG	ACG	TTC	CGG	ATC	AGC	GTT	TAT	633
Tyr	Ile	Arg	Glu	Arg	Phe	Asp	Asn	Glu	Thr	Phe	Arg	Ile	Ser	Val	Tyr	
180					185					190					195	
CAG	GTG	CTC	CAG	GAG	CAC	TTG	GGC	AGG	GAA	TCG	GAT	CTC	TTC	CTG	CTC	681
Gln	Val	Leu	Gln	Glu	His	Leu	Gly	Arg	Glu	Ser	Asp	Leu	Phe	Leu	Leu	
				200					205					210		
GAC	AGC	CGT	ACC	CTC	TGG	GCC	TCG	GAG	GAG	GGC	TGG	CTG	GTG	TTT	GAC	729
Asp	Ser	Arg	Thr	Leu	Trp	Ala	Ser	Glu	Glu	Gly	Trp	Leu	Val	Phe	Asp	
		215						220					225			
ATC	ACA	GCC	ACC	AGC	AAC	CAC	TGG	GTG	GTC	AAT	CCG	CGG	CAC	AAC	CTG	777
Ile	Thr	Ala	Thr	Ser	Asn	His	Trp	Val	Val	Asn	Pro	Arg	His	Asn	Leu	
		230					235					240				
GGC	CTG	CAG	CTC	TCG	GTG	GAG	ACG	CTG	GAT	GGG	CAG	AGC	ATC	AAC	CCC	825
Gly	Leu	Gln	Leu	Ser	Val	Glu	Thr	Leu	Asp	Gly	Gln	Ser	Ile	Asn	Pro	
	245					250					255					
AAG	TTG	GCG	GGC	CTG	ATT	GGG	CGG	CAC	GGG	CCC	CAG	AAC	AAG	CAG	CCC	873
Lys	Leu	Ala	Gly	Leu	Ile	Gly	Arg	His	Gly	Pro	Gln	Asn	Lys	Gln	Pro	
260					265					270					275	

TTC	ATG	GTG	GCT	TTC	TTC	AAG	GCC	ACG	GAG	GTC	CAC	TTC	CGC	AGC	ATC	921				
Phe	Met	Val	Ala	Phe	Phe	Lys	Ala	Thr	Glu	Val	His	Phe	Arg	Ser	Ile					
				280					285					290						
CGG	TCC	ACG	GGG	AGC	AAA	CAG	CGC	AGC	CAG	AAC	CGC	TCC	AAG	ACG	CCC	969				
Arg	Ser	Thr	Gly	Ser	Lys	Gln	Arg	Ser	Gln	Asn	Arg	Ser	Lys	Thr	Pro					
			295					300					305							
AAG	AAC	CAG	GAA	GCC	CTG	CGG	ATG	GCC	AAC	GTG	GCA	GAG	AAC	AGC	AGC	1017				
Lys	Asn	Gln	Glu	Ala	Leu	Arg	Met	Ala	Asn	Val	Ala	Glu	Asn	Ser	Ser					
		310					315					320								
AGC	GAC	CAG	AGG	CAG	GCC	TGT	AAG	AAG	CAC	GAG	CTG	TAT	GTC	AGC	TTC	1065				
Ser	Asp	Gln	Arg	Gln	Ala	Cys	Lys	Lys	His	Glu	Leu	Tyr	Val	Ser	Phe					
	325					330					335									
CGA	GAC	CTG	GGC	TGG	CAG	GAC	TGG	ATC	ATC	GCG	CCT	GAA	GGC	TAC	GCC	1113				
Arg	Asp	Leu	Gly	Trp	Gln	Asp	Trp	Ile	Ile	Ala	Pro	Glu	Gly	Tyr	Ala					
	340				345					350					355					
GCC	TAC	TAC	TGT	GAG	GGG	GAG	TGT	GCC	TTC	CCT	CTG	AAC	TCC	TAC	ATG	1161				
Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ala	Phe	Pro	Leu	Asn	Ser	Tyr	Met					
			360					365						370						
AAC	GCC	ACC	AAC	CAC	GCC	ATC	GTG	CAG	ACG	CTG	GTC	CAC	TTC	ATC	AAC	1209				
Asn	Ala	Thr	Asn	His	Ala	Ile	Val	Gln	Thr	Leu	Val	His	Phe	Ile	Asn					
			375					380					385							
CCG	GAA	ACG	GTG	CCC	AAG	CCC	TGC	TGT	GCG	CCC	ACG	CAG	CTC	AAT	GCC	1257				
Pro	Glu	Thr	Val	Pro	Lys	Pro	Cys	Cys	Ala	Pro	Thr	Gln	Leu	Asn	Ala					
		390					395					400								
ATC	TCC	GTC	CTC	TAC	TTC	GAT	GAC	AGC	TCC	AAC	GTC	ATC	CTG	AAG	AAA	1305				
Ile	Ser	Val	Leu	Tyr	Phe	Asp	Asp	Ser	Ser	Asn	Val	Ile	Leu	Lys	Lys					
	405					410					415									
TAC	AGA	AAC	ATG	GTG	GTC	CGG	GCC	TGT	GGC	TGC	CAC	TAGCTCCTCC				1351				
Tyr	Arg	Asn	Met	Val	Val	Arg	Ala	Cys	Gly	Cys	His									
	420				425				430											
GAGAATTCAG ACCCTTTGGG GCCAAGTTTT TCTGGATCCT CCATTGCTCG CCTTGGCCAG																1411				
GAACCAGCAG ACCAACTGCC TTTTGTGAGA CCTTCCCCTC CCTATCCCCA ACTTTAAAGG																1471				
TGTGAGAGTA TTAGGAAACA TGAGCAGCAT ATGGCTTTTG ATCAGTTTTT CAGTGGCAGC																1531				
ATCCAATGAA CAAGATCCTA CAAGCTGTGC AGGCAAAACC TAGCAGGAAA AAAAAACAAC																1591				
GCATAAAGAA AAATGGCCGG GCCAGGTCAT TGGCTGGGAA GTCTCAGCCA TGCACGGACT																1651				
CGTTTCCAGA GGTAATTATG AGCGCCTACC AGCCAGGCCA CCCAGCCGTG GGAGGAAGGG																1711				
GGCGTGGCAA GGGGTGGGCA CATTGGTGTG TGTGCGAAAG GAAAATTGAC CCGGAAGTTC																1771				
CTGTAATAAA TGTCACAATA AAACGAATGA ATGAAAAAAAA AAAAAAAAAA A																1822				

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 431 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(D) OTHER INFORMATION: /Product="OP1-PP"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```

Met His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala
 1           5           10           15
Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser
          20           25           30
Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser
          35           40           45
Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu
          50           55           60
Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro
          65           70           75           80
Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly
          85           90           95
Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser
          100          105          110
Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr
          115          120          125
Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys
          130          135          140
Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu
          145          150          155          160
Ser Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile
          165          170          175
Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile
          180          185          190
Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp L u
          195          200          205

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Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu
 210 215 220
 Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg
 225 230 235 240
 His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser
 245 250 255
 Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn
 260 265 270
 Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe
 275 280 285
 Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser
 290 295 300
 Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met' Ala Asn Val Ala Glu
 305 310 315 320
 Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr
 325 330 335
 Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu
 340 345 350
 Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn
 355 360 365
 Ser Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His
 370 375 380
 Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln
 385 390 395 400
 Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile
 405 410 415
 Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
 420 425 430

SUBSTITUTE SHEET

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1873 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: MURIDAE
- (F) TISSUE TYPE: EMBRYO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 104..1393
- (D) OTHER INFORMATION: /note= "MOP1 (CDNA)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTGCAGCAAG TGACCTCGGG TCGTGGACCG CTGCCCTGCC CCCTCCGCTG CCACCTGGGG	60
CGGCGCGGGC CCGGTGCCCC GGATCGCGCG TAGAGCCGGC GCG ATG CAC GTG CGC	115
Met His Val Arg	
1	
TCG CTG CGC GCT GCG GCG CCA CAC AGC TTC GTG GCG CTC TGG GCG CCT	163
Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala Pro	
5 10 15 20	
CTG TTC TTG CTG CGC TCC GCC CTG GCC GAT TTC AGC CTG GAC AAC GAG	211
Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn Glu	
25 30 35	
GTG CAC TCC AGC TTC ATC CAC CGG CGC CTC CGC AGC CAG GAG CGG CGG	259
Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg Arg	
40 45 50	
GAG ATG CAG CGG GAG ATC CTG TCC ATC TTA GGG TTG CCC CAT CGC CCG	307
Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg Pro	
55 60 65	
CGC CCG CAC CTC CAG GGA AAG CAT AAT TCG GCG CCC ATG TTC ATG TTG	355
Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met Leu	
70 75 80	
GAC CTG TAC AAC GCC ATG GCG GTG GAG GAG AGC GGG CCG GAC GGA CAG	403
Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Ser Gly Pro Asp Gly Gln	
85 90 95 100	

GGC	TTC	TCC	TAC	CCC	TAC	AAG	GCC	GTC	TTC	AGT	ACC	CAG	GGC	CCC	CCT	451
Gly	Phe	Ser	Tyr	Pro	Tyr	Lys	Ala	Val	Phe	Ser	Thr	Gln	Gly	Pro	Pro	
				105					110					115		
TTA	GCC	AGC	CTG	CAG	GAC	AGC	CAT	TTC	CTC	ACT	GAC	GCC	GAC	ATG	GTC	499
Leu	Ala	Ser	Leu	Gln	Asp	Ser	His	Phe	Leu	Thr	Asp	Ala	Asp	Met	Val	
			120					125					130			
ATG	AGC	TTC	GTC	AAC	CTA	GTG	GAA	CAT	GAC	AAA	GAA	TTC	TTC	CAC	CCT	547
Met	Ser	Phe	Val	Asn	Leu	Val	Glu	His	Asp	Lys	Glu	Phe	Phe	His	Pro	
		135					140					145				
CGA	TAC	CAC	CAT	CGG	GAG	TTC	CGG	TTT	GAT	CTT	TCC	AAG	ATC	CCC	GAG	595
Arg	Tyr	His	His	Arg	Glu	Phe	Arg	Phe	Asp	Leu	Ser	Lys	Ile	Pro	Glu	
	150					155					160					
GGC	GAA	CGG	GTG	ACC	GCA	GCC	GAA	TTC	AGG	ATC	TAT	AAG	GAC	TAC	ATC	643
Gly	Glu	Arg	Val	Thr	Ala	Ala	Glu	Phe	Arg	Ile	Tyr	Lys	Asp	Tyr	Ile	
	165				170					175					180	
CGG	GAG	CGA	TTT	GAC	AAC	GAG	ACC	TTC	CAG	ATC	ACA	GTC	TAT	CAG	GTG	691
Arg	Glu	Arg	Phe	Asp	Asn	Glu	Thr	Phe	Gln	Ile	Thr	Val	Tyr	Gln	Val	
				185					190					195		
CTC	CAG	GAG	CAC	TCA	GGC	AGG	GAG	TCG	GAC	CTC	TTC	TTG	CTG	GAC	AGC	739
Leu	Gln	Glu	His	Ser	Gly	Arg	Glu	Ser	Asp	Leu	Phe	Leu	Leu	Asp	Ser	
			200					205					210			
CGC	ACC	ATC	TGG	GCT	TCT	GAG	GAG	GGC	TGG	TTG	GTG	TTT	GAT	ATC	ACA	787
Arg	Thr	Ile	Trp	Ala	Ser	Glu	Glu	Gly	Trp	Leu	Val	Phe	Asp	Ile	Thr	
		215					220					225				
GCC	ACC	AGC	AAC	CAC	TGG	GTG	GTC	AAC	CCT	CGG	CAC	AAC	CTG	GGC	TTA	835
Ala	Thr	Ser	Asn	His	Trp	Val	Val	Asn	Pro	Arg	His	Asn	Leu	Gly	Leu	
	230					235					240					
CAG	CTC	TCT	GTG	GAG	ACC	CTG	GAT	GGG	CAG	AGC	ATC	AAC	CCC	AAG	TTG	883
Gln	Leu	Ser	Val	Glu	Thr	Leu	Asp	Gly	Gln	Ser	Ile	Asn	Pro	Lys	Leu	
	245				250					255					260	
GCA	GGC	CTG	ATT	GGA	CGG	CAT	GGA	CCC	CAG	AAC	AAG	CAA	CCC	TTC	ATG	931
Ala	Gly	Leu	Ile	Gly	Arg	His	Gly	Pro	Gln	Asn	Lys	Gln	Pro	Phe	Met	
				265					270					275		
GTG	GCC	TTC	TTC	AAG	GCC	ACG	GAA	GTC	CAT	CTC	CGT	AGT	ATC	CGG	TCC	979
Val	Ala	Phe	Phe	Lys	Ala	Thr	Glu	Val	His	Leu	Arg	Ser	Ile	Arg	Ser	
			280					285					290			
ACG	GGG	GGC	AAG	CAG	CGC	AGC	CAG	AAT	CGC	TCC	AAG	ACG	CCA	AAG	AAC	1027
Thr	Gly	Gly	Lys	Gln	Arg	Ser	Gln	Asn	Arg	Ser	Lys	Thr	Pro	Lys	Asn	
		295					300					305				
CAA	GAG	GCC	CTG	AGG	ATG	GCC	AGT	GTG	GCA	GAA	AAC	AGC	AGC	AGT	GAC	1075
Gln	Glu	Ala	Leu	Arg	Met	Ala	Ser	Val	Ala	Glu	Asn	Ser	Ser	Ser	Asp	
	310					315					320					

CAG AGG CAG GCC TGC AAG AAA CAT GAG CTG TAC GTC AGC TTC CGA GAC Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp 325 330 335 340	1123
CTT GGC TGG CAG GAC TGG ATC ATT GCA CCT GAA GGC TAT GCT GCC TAC Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Tyr 345 350 355	1171
TAC TGT GAG GGA GAG TGC GCC TTC CCT CTG AAC TCC TAC ATG AAC GCC Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn Ala 360 365 370	1219
ACC AAC CAC GCC ATC GTC CAG ACA CTG GTT CAC TTC ATC AAC CCA GAC Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn Pro Asp 375 380 385	1267
ACA GTA CCC AAG CCC TGC TGT GCG CCC ACC CAG CTC AAC GCC ATC TCT Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile Ser 390 395 400	1315
GTC CTC TAC TTC GAC GAC AGC TCT AAT GTC ATC CTG AAG AAG TAC AGA Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg 405 410 415 420	1363
AAC ATG GTG GTC CGG GCC TGT GGC TGC CAC TAGCTCTTCC TGAGACCCTG Asn Met Val Val Arg Ala Cys Gly Cys His 425 430	1413
ACCTTTGCGG GGCCACACCT TTCCAAATCT TCGATGTCTC ACCATCTAAG TCTCTCACTG	1473
CCCACCTTGG CGAGGAGAAC AGACCAACCT CTCCTGAGCC TTCCCTCACC TCCCAACCGG	1533
AAGCATGTAA GGGTTCCAGA AACCTGAGCG TGCAGCAGCT GATGAGCGCC CTTTCCTTCT	1593
GGCACGTGAC GGACAAGATC CTACCAGCTA CCACAGCAAA CGCCTAAGAG CAGGAAAAAT	1653
GTCTGCCAGG AAAGTGTCCA GTGTCCACAT GGCCCTGGC GCTCTGAGTC TTTGAGGAGT	1713
AATCGCAAGC CTCGTTTCAGC TGCAGCAGAA GGAAGGGCTT AGCCAGGGTG GGCGCTGGCG	1773
TCTGTGTTGA AGGGAAACCA AGCAGAAGCC ACTGTAATGA TATGTCACAA TAAAACCCAT	1833
GAATGAAAAA AAAAAAAAAA AAAAAAAAAA AAAAGAATTC	1873

20) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (D) OTHER INFORMATION: /product= "mOP1-PP"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```

Met His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala
 1           5           10           15
Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser
          20           25           30
Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser
          35           40           45
Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu
          50           55           60
Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro
 65           70           75           80
Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Ser Gly
          85           90           95
Pro Asp Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr
          100          105          110
Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp
          115          120          125
Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys Glu
          130          135          140
Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser
          145          150          155          160
Lys Ile Pro Glu Gly Glu Arg Val Thr Ala Ala Glu Phe Arg Ile Tyr
          165          170          175
Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Gln Ile Thr
          180          185          190
Val Tyr Gln Val Leu Gln Glu His Ser Gly Arg Glu Ser Asp Leu Phe
          195          200          205

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Leu Leu Asp Ser Arg Thr Ile Trp Ala Ser Glu Glu Gly Trp Leu Val
 210 215 220
 Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg His
 225 230 235 240
 Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile
 245 250 255
 Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys
 260 265 270
 Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Leu Arg
 275 280 285
 Ser Ile Arg Ser Thr Gly Gly Lys Gln Arg Ser Gln Asn Arg Ser Lys
 290 295 300
 Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Ser Val Ala Glu Asn
 305 310 315 320
 Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val
 325 330 335
 Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly
 340 345 350
 Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser
 355 360 365
 Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe
 370 375 380
 Ile Asn Pro Asp Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu
 385 390 395 400
 Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu
 405 410 415
 Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
 420 425 430

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1723 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (F) TISSUE TYPE: HIPPOCAMPUS

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 490..1696
- (D) OTHER INFORMATION: /note= "hOP2 (cDNA)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

GGCGCCGGCA GAGCAGGAGT GGCTGGAGGA GCTGTGGTTG GAGCAGGAGG TGGCACGGCA      60
GGGCTGGAGG GCTCCCTATG AGTGGCGGAG ACGGCCCAGG AGGCGCTGGA GCAACAGCTC      120
CCACACCGCA CCAAGCGGTG GCTGCAGGAG CTCGCCCATC GCCCCTGCGC TGCTCGGACC      180
CGGGCCACAG CCGGACTGGC GGGTACGGCG GCGACAGAGG CATTGGCCGA GAGTCCCAGT      240
CCGCAGAGTA GCCCCGGCCT CGAGGCGGTG GCGTCCCGGT CCTCTCCGTC CAGGAGCCAG      300
GACAGGTGTC GCGCGGCGGG GCTCCAGGGA CCGCGCCTGA GGCCGGCTGC CCGCCCGTCC      360
CGCCCCGCCC CGCCGCCCCG CGCCCGCCGA GCCCAGCCTC CTTGCCGTCG GGGCGTCCCC      420
AGGCCCTGGG TCGGCCGCGG AGCCGATGCG CGCCCGCTGA GCGCCCCAGC TGAGCGCCCC      480
CGGCCTGCC ATG ACC GCG CTC CCC GGC CCG CTC TGG CTC CTG GGC CTG      528
      Met Thr Ala Leu Pro Gly Pro Leu Trp Leu Leu Gly Leu
          1             5             10

GCG CTA TGC GCG CTG GGC GGG GGC GGC CCC GGC CTG CGA CCC CCG CCC      576
Ala Leu Cys Ala Leu Gly Gly Gly Gly Pro Gly Leu Arg Pro Pro Pro
      15             20             25

GGC TGT CCC CAG CGA CGT CTG GGC GCG CGC GAG CGC CGG GAC GTG CAG      624
Gly Cys Pro Gln Arg Arg Leu Gly Ala Arg Glu Arg Arg Asp Val Gln
      30             35             40             45

CGC GAG ATC CTG GCG GTG CTC GGG CTG CCT GGG CGG CCC CGG CCC CGC      672
Arg Glu Ile Leu Ala Val Leu Gly Leu Pro Gly Arg Pro Arg Pro Arg
          50             55             60

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GCG CCA CCC GCC GCC TCC CGG CTG CCC GCG TCC GCG CCG CTC TTC ATG	720
Ala Pro Pro Ala Ala Ser Arg Leu Pro Ala Ser Ala Pro Leu Phe Met	
65 70 75	
CTG GAC CTG TAC CAC GCC ATG GCC GGC GAC GAC GAC GAG GAC GGC GCG	768
Leu Asp Leu Tyr His Ala Met Ala Gly Asp Asp Asp Glu Asp Gly Ala	
80 85 90	
CCC GCG GAG CGG CGC CTG GGC CGC GCC GAC CTG GTC ATG AGC TTC GTT	816
Pro Ala Glu Arg Arg Leu Gly Arg Ala Asp Leu Val Met Ser Phe Val	
95 100 105	
AAC ATG GTG GAG CGA GAC CGT GCC CTG GGC CAC CAG GAG CCC CAT TGG	864
Asn Met Val Glu Arg Asp Arg Ala Leu Gly His Gln Glu Pro His Trp	
110 115 120 125	
AAG GAG TTC CGC TTT GAC CTG ACC CAG ATC CCG GCT GGG GAG GCG GTC	912
Lys Glu Phe Arg Phe Asp Leu Thr Gln Ile Pro Ala Gly Glu Ala Val	
130 135 140	
ACA GCT GCG GAG TTC CGG ATT TAC AAG GTG CCC AGC ATC CAC CTG CTC	960
Thr Ala Ala Glu Phe Arg Ile Tyr Lys Val Pro Ser Ile His Leu Leu	
145 150 155	
AAC AGG ACC CTC CAC GTC AGC ATG TTC CAG GTG GTC CAG GAG CAG TCC	1008
Asn Arg Thr Leu His Val Ser Met Phe Gln Val Val Gln Glu Gln Ser	
160 165 170	
AAC AGG GAG TCT GAC TTG TTC TTT TTG GAT CTT CAG ACG CTC CGA GCT	1056
Asn Arg Glu Ser Asp Leu Phe Phe Leu Asp Leu Gln Thr Leu Arg Ala	
175 180 185	
GGA GAC GAG GGC TGG CTG GTG CTG GAT GTC ACA GCA GCC AGT GAC TGC	1104
Gly Asp Glu Gly Trp Leu Val Leu Asp Val Thr Ala Ala Ser Asp Cys	
190 195 200 205	
TGG TTG CTG AAG CGT CAC AAG GAC CTG GGA CTC CGC CTC TAT GTG GAG	1152
Trp Leu Leu Lys Arg His Lys Asp Leu Gly Leu Arg Leu Tyr Val Glu	
210 215 220	
ACT GAG GAC GGG CAC AGC GTG GAT CCT GGC CTG GCC GGC CTG CTG GGT	1200
Thr Glu Asp Gly His Ser Val Asp Pro Gly Leu Ala Gly Leu Leu Gly	
225 230 235	
CAA CGG GCC CCA CGC TCC CAA CAG CCT TTC GTG GTC ACT TTC TTC AGG	1248
Gln Arg Ala Pro Arg Ser Gln Gln Pro Phe Val Val Thr Phe Phe Arg	
240 245 250	
GCC AGT CCG AGT CCC ATC CGC ACC CCT CGG GCA GTG AGG CCA CTG AGG	1296
Ala Ser Pro Ser Pro Ile Arg Thr Pro Arg Ala Val Arg Pro Leu Arg	
255 260 265	

AGG	AGG	CAG	CCG	AAG	AAA	AGC	AAC	GAG	CTG	CCG	CAG	GCC	AAC	CGA	CTC	1344
Arg	Arg	Gln	Pro	Lys	Lys	Ser	Asn	Glu	Leu	Pro	Gln	Ala	Asn	Arg	Leu	
270					275					280					285	
CCA	GGG	ATC	TTT	GAT	GAC	GTC	CAC	GGC	TCC	CAC	GGC	CGG	CAG	GTC	TGC	1392
Pro	Gly	Ile	Phe	Asp	Asp	Val	His	Gly	Ser	His	Gly	Arg	Gln	Val	Cys	
				290					295					300		
CGT	CGG	CAC	GAG	CTC	TAC	GTC	AGC	TTC	CAG	GAC	CTC	GGC	TGG	CTG	GAC	1440
Arg	Arg	His	Glu	Leu	Tyr	Val	Ser	Phe	Gln	Asp	Leu	Gly	Trp	Leu	Asp	
			305					310					315			
TGG	GTC	ATC	GCT	CCC	CAA	GGC	TAC	TCG	GCC	TAT	TAC	TGT	GAG	GGG	GAG	1488
Trp	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser	Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	
		320					325					330				
TGC	TCC	TTC	CCA	CTG	GAC	TCC	TGC	ATG	AAT	GCC	ACC	AAC	CAC	GCC	ATC	1536
Cys	Ser	Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	Ala	Thr	Asn	His	Ala	Ile	
	335					340					345					
CTG	CAG	TCC	CTG	GTG	CAC	CTG	ATG	AAG	CCA	AAC	GCA	GTC	CCC	AAG	GCG	1584
Leu	Gln	Ser	Leu	Val	His	Leu	Met	Lys	Pro	Asn	Ala	Val	Pro	Lys	Ala	
350					355					360					365	
TGC	TGT	GCA	CCC	ACC	AAG	CTG	AGC	GCC	ACC	TCT	GTG	CTC	TAC	TAT	GAC	1632
Cys	Cys	Ala	Pro	Thr	Lys	Leu	Ser	Ala	Thr	Ser	Val	Leu	Tyr	Tyr	Asp	
				370					375					380		
AGC	AGC	AAC	AAC	GTC	ATC	CTG	CGC	AAA	CAC	CGC	AAC	ATG	GTG	GTC	AAG	1680
Ser	Ser	Asn	Asn	Val	Ile	Leu	Arg	Lys	His	Arg	Asn	Met	Val	Val	Lys	
			385					390					395			
GCC	TGC	GGC	TGC	CAC	T	GAGTCAGCCC	GCCCAGCCCT	ACTGCAG								1723
Ala	Cys	Gly	Cys	His												
		400														

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) OTHER INFORMATION: /product= "hOP2-PP"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```

Met Thr Ala Leu Pro Gly Pro Leu Trp Leu Leu Gly Leu Ala Leu Cys
 1           5           10           15
Ala Leu Gly Gly Gly Gly Pro Gly Leu Arg Pro Pro Pro Gly Cys Pro
          20           25           30
Gln Arg Arg Leu Gly Ala Arg Glu Arg Arg Asp Val Gln Arg Glu Ile
          35           40           45
Leu Ala Val Leu Gly Leu Pro Gly Arg Pro Arg Pro Arg Ala Pro Pro
          50           55           60
Ala Ala Ser Arg Leu Pro Ala Ser Ala Pro Leu Phe Met Leu Asp Leu
          65           70           75           80
Tyr His Ala Met Ala Gly Asp Asp Asp Glu Asp Gly Ala Pro Ala Glu
          85           90           95
Arg Arg Leu Gly Arg Ala Asp Leu Val Met Ser Phe Val Asn Met Val
          100          105          110
Glu Arg Asp Arg Ala Leu Gly His Gln Glu Pro His Trp Lys Glu Phe
          115          120          125
Arg Phe Asp Leu Thr Gln Ile Pro Ala Gly Glu Ala Val Thr Ala Ala
          130          135          140
Glu Phe Arg Ile Tyr Lys Val Pro Ser Ile His Leu Leu Asn Arg Thr
          145          150          155          160
Leu His Val Ser Met Phe Gln Val Val Gln Glu Gln Ser Asn Arg Glu
          165          170          175
Ser Asp Leu Phe Phe Leu Asp Leu Gln Thr Leu Arg Ala Gly Asp Glu
          180          185          190
Gly Trp Leu Val Leu Asp Val Thr Ala Ala Ser Asp Cys Trp Leu Leu
          195          200          205

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Lys Arg His Lys Asp Leu Gly Leu Arg Leu Tyr Val Glu Thr Glu Asp
 210 215 220
 Gly His Ser Val Asp Pro Gly Leu Ala Gly Leu Leu Gly Gln Arg Ala
 225 230 235 240
 Pro Arg Ser Gln Gln Pro Phe Val Val Thr Phe Phe Arg Ala Ser Pro
 245 250 255
 Ser Pro Ile Arg Thr Pro Arg Ala Val Arg Pro Leu Arg Arg Arg Gln
 260 265 270
 Pro Lys Lys Ser Asn Glu Leu Pro Gln Ala Asn Arg Leu Pro Gly Ile
 275 280 285
 Phe Asp Asp Val His Gly Ser His Gly Arg Gln Val Cys Arg Arg His
 290 295 300
 Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu Asp Trp Val Ile
 305 310 315
 Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr Cys Glu Gly Glu Cys Ser Phe
 325 330 335
 Pro Leu Asp Ser Cys Met Asn Ala Thr Asn His Ala Ile Leu Gln Ser
 340 345 350
 Leu Val His Leu Met Lys Pro Asn Ala Val Pro Lys Ala Cys Cys Ala
 355 360 365
 Pro Thr Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp Ser Ser Asn
 370 375 380
 Asn Val Ile Leu Arg Lys His Arg Asn Met Val Val Lys Ala Cys Gly
 385 390 395 400
 Cys His

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1926 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: MURIDAE
 (F) TISSUE TYPE: EMBRYO

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 93..1289
 (D) OTHER INFORMATION: /note= "mOP2 cDNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```

GCCAGGCACA GGTGCGCCGT CTGGTCCTCC CCGTCTGGCG TCAGCCGAGC      50
CCGACCAGCT ACCAGTGGAT GCGCGCCGGC TGAAAGTCCG AG ATG GCT ATG CGT      104
                                     Met Ala Met Arg
                                     1
CCC GGG CCA CTC TGG CTA TTG GGC CTT GCT CTG TGC GCG CTG GGA GGC      152
Pro Gly Pro Leu Trp Leu Leu Gly Leu Ala Leu Cys Ala Leu Gly Gly
  5                10                15                20
GGC CAC GGT CCG CGT CCC CCG CAC ACC TGT CCC CAG CGT CGC CTG GGA      200
Gly His Gly Pro Arg Pro Pro His Thr Cys Pro Gln Arg Arg Leu Gly
                25                30                35
GCG CGC GAG CGC CGC GAC ATG CAG CGT GAA ATC CTG GCG GTG CTC GGG      248
Ala Arg Glu Arg Arg Asp Met Gln Arg Glu Ile Leu Ala Val Leu Gly
                40                45                50
CTA CCG GGA CGG CCC CGA CCC CGT GCA CAA CCC GCG GCT GCC CGG CAG      296
Leu Pro Gly Arg Pro Arg Pro Arg Ala Gln Pro Ala Ala Ala Arg Gln
                55                60                65
CCA GCG TCC GCG CCC CTC TTC ATG TTG GAC CTA TAC CAC GCC ATG ACC      344
Pro Ala Ser Ala Pro Leu Phe Met Leu Asp Leu Tyr His Ala Met Thr
                70                75                80
GAT GAC GAC GAC GGC GGG CCA CCA CAG GCT CAC TTA GGC CGT GCC GAC      392
Asp Asp Asp Asp Gly Gly Pro Pro Gln Ala His Leu Gly Arg Ala Asp
  85                90                95                100

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CTG	GTC	ATG	AGC	TTC	GTC	AAC	ATG	GTG	GAA	CGC	GAC	CGT	ACC	CTG	GGC	440
Leu	Val	Met	Ser	Phe	Val	Asn	Met	Val	Glu	Arg	Asp	Arg	Thr	Leu	Gly	
				105					110					115		
TAC	CAG	GAG	CCA	CAC	TGG	AAG	GAA	TTC	CAC	TTT	GAC	CTA	ACC	CAG	ATC	488
Tyr	Gln	Glu	Pro	His	Trp	Lys	Glu	Phe	His	Phe	Asp	Leu	Thr	Gln	Ile	
			120					125					130			
CCT	GCT	GGG	GAG	GCT	GTC	ACA	GCT	GCT	GAG	TTC	CGG	ATC	TAC	AAA	GAA	536
Pro	Ala	Gly	Glu	Ala	Val	Thr	Ala	Ala	Glu	Phe	Arg	Ile	Tyr	Lys	Glu	
		135					140					145				
CCC	AGC	ACC	CAC	CCG	CTC	AAC	ACA	ACC	CTC	CAC	ATC	AGC	ATG	TTC	GAA	584
Pro	Ser	Thr	His	Pro	Leu	Asn	Thr	Thr	Leu	His	Ile	Ser	Met	Phe	Glu	
	150					155					160					
GTG	GTC	CAA	GAG	CAC	TCC	AAC	AGG	GAG	TCT	GAC	TTG	TTC	TTT	TTG	GAT	632
Val	Val	Gln	Glu	His	Ser	Asn	Arg	Glu	Ser	Asp	Leu	Phe	Phe	Leu	Asp	
165					170					175					180	
CTT	CAG	ACG	CTC	CGA	TCT	GGG	GAC	GAG	GGC	TGG	CTG	GTG	CTG	GAC	ATC	680
Leu	Gln	Thr	Leu	Arg	Ser	Gly	Asp	Glu	Gly	Trp	Leu	Val	Leu	Asp	Ile	
				185					190					195		
ACA	GCA	GCC	AGT	GAC	CGA	TGG	CTG	CTG	AAC	CAT	CAC	AAG	GAC	CTG	GGA	728
Thr	Ala	Ala	Ser	Asp	Arg	Trp	Leu	Leu	Asn	His	His	Lys	Asp	Leu	Gly	
			200				205						210			
CTC	CGC	CTC	TAT	GTG	GAA	ACC	GCG	GAT	GGG	CAC	AGC	ATG	GAT	CCT	GGC	776
Leu	Arg	Leu	Tyr	Val	Glu	Thr	Ala	Asp	Gly	His	Ser	Met	Asp	Pro	Gly	
		215					220					225				
CTG	GCT	GGT	CTG	CTT	GGA	CGA	CAA	GCA	CCA	CGC	TCC	AGA	CAG	CCT	TTC	824
Leu	Ala	Gly	Leu	Leu	Gly	Arg	Gln	Ala	Pro	Arg	Ser	Arg	Gln	Pro	Phe	
	230					235					240					
ATG	GTA	ACC	TTC	TTC	AGG	GCC	AGC	CAG	AGT	CCT	GTG	CGG	GCC	CCT	CGG	872
Met	Val	Thr	Phe	Phe	Arg	Ala	Ser	Gln	Ser	Pro	Val	Arg	Ala	Pro	Arg	
245					250					255					260	
GCA	GCG	AGA	CCA	CTG	AAG	AGG	AGG	CAG	CCA	AAG	AAA	ACG	AAC	GAG	CTT	920
Ala	Ala	Arg	Pro	Leu	Lys	Arg	Arg	Gln	Pro	Lys	Lys	Thr	Asn	Glu	Leu	
				265					270					275		
CCG	CAC	CCC	AAC	AAA	CTC	CCA	GGG	ATC	TTT	GAT	GAT	GGC	CAC	GGT	TCC	968
Pro	His	Pro	Asn	Lys	Leu	Pro	Gly	Ile	Phe	Asp	Asp	Gly	His	Gly	Ser	
			280					285					290			
CGC	GGC	AGA	GAG	GTT	TGC	CGC	AGG	CAT	GAG	CTC	TAC	GTC	AGC	TTC	CGT	1016
Arg	Gly	Arg	Glu	Val	Cys	Arg	Arg	His	Glu	Leu	Tyr	Val	Ser	Phe	Arg	
		295					300					305				

GAC CTT GGC TGG CTG GAC TGG GTC ATC GCC CCC CAG GGC TAC TCT GCC Asp Leu Gly Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala 310 315 320	1064
TAT TAC TGT GAG GGG GAG TGT GCT TTC CCA CTG GAC TCC TGT ATG AAC Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asp Ser Cys Met Asn 325 330 335 340	1112
GCC ACC AAC CAT GCC ATC TTG CAG TCT CTG GTG CAC CTG ATG AAG CCA Ala Thr Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met Lys Pro 345 350 355	1160
GAT GTT GTC CCC AAG GCA TGC TGT GCA CCC ACC AAA CTG AGT GCC ACC Asp Val Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr 360 365 370	1208
TCT GTG CTG TAC TAT GAC AGC AGC AAC AAT GTC ATC CTG CGT AAA CAC Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His 375 380 385	1256
CGT AAC ATG GTG GTC AAG GCC TGT GGC TGC CAC TGAGGCCCCG CCCAGCATCC Arg Asn Met Val Val Lys Ala Cys Gly Cys His 390 395	1309
TGCTTCTACT ACCTTACCAT CTGGCCGGGC CCCTCTCCAG AGGCAGAAAC CCTTCTATGT	1369
TATCATAGCT CAGACAGGGG CAATGGGAGG CCCTTCACTT CCCCTGGCCA CTTCTTGCTA	1429
AAATTCTGGT CTTTCCCAGT TCCTCTGTCC TTCATGGGGT TTCGGGGCTA TCACCCCGCC	1489
CTCTCCATCC TCCTACCCCA AGCATAGACT GAATGCACAC AGCATCCCAG AGCTATGCTA	1549
ACTGAGAGGT CTGGGGTCAG CACTGAAGGC CCACATGAGG AAGACTGATC CTTGGCCATC	1609
CTCAGCCCAC AATGGCAAAT TCTGGATGGT CTAAGAAGGC CGTGGAATTC TAACTAGAT	1669
GATCTGGGCT CTCTGCACCA TTCATTGTGG CAGTTGGGAC ATTTTtagGT ATAACAGACA	1729
CATACACTTA GATCAATGCA TCGCTGTACT CTTGAAATC AGAGCTAGCT TGTTAGAAAA	1789
AGAATCAGAG CCAGGTATAG CGGTGCATGT CATTAATCCC AGCGCTAAAG AGACAGAGAC	1849
AGGAGAATCT CTGTGAGTTC AAGGCCACAT AGAAAGAGCC TGTCTCGGGA GCAGGAAAAA	1909
AAAAAAAAAC GGAATTC	1926

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (D) OTHER INFORMATION: /product= "mOP2-PP"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```

Met Ala Met Arg Pro Gly Pro Leu Trp Leu Leu Gly Leu Ala Leu Cys
 1           5           10           15
Ala Leu Gly Gly Gly His Gly Pro Arg Pro Pro His Thr Cys Pro Gln
          20           25           30
Arg Arg Leu Gly Ala Arg Glu Arg Arg Asp Met Gln Arg Glu Ile Leu Ala
          35           40           45
Val Leu Gly Leu Pro Gly Arg Pro Arg Pro Arg Ala Gln Pro Ala Ala
          50           55           60           65
Ala Arg Gln Pro Ala Ser Ala Pro Leu Phe Met Leu Asp Leu Tyr His Ala
          70           75           80
Met Thr Asp Asp Asp Asp Gly Gly Pro Pro Gln Ala His Leu Gly Arg
          85           90           95
Ala Asp Leu Val Met Ser Phe Val Asn Met Val Glu Arg Asp Arg Thr
          100          105          110
Leu Gly Tyr Gln Glu Pro His Trp Lys Glu Phe His Phe Asp Leu Thr
          115          120          125          130
Gln Ile Pro Ala Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr
          135          140          145
Lys Glu Pro Ser Thr His Pro Leu Asn Thr Thr Leu His Ile Ser Met
          150          155          160
Phe Glu Val Val Gln Glu His Ser Asn Arg Glu Ser Asp Leu Phe Phe
          165          170          175
Leu Asp Leu Gln Thr Leu Arg Ser Gly Asp Glu Gly Trp Leu Val Leu
          180          185          190
Asp Ile Thr Ala Ala Ser Asp Arg Trp Leu Leu Asn His His Lys Asp
          195          200          205          210

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Leu Gly Leu Arg Leu Tyr Val Glu Thr Ala Asp Gly His Ser Met Asp
 215 220 225
 Pro Gly Leu Ala Gly Leu Leu Gly Arg Gln Ala Pro Arg Ser Arg Gln
 230 235 240
 Pro Phe Met Val Thr Phe Phe Arg Ala Ser Gln Ser Pro Val Arg Ala
 245 250 255
 Pro Arg Ala Ala Arg Pro Leu Lys Arg Arg Gln Pro Lys Lys Thr Asn
 260 265 270
 Glu Leu Pro His Pro Asn Lys Leu Pro Gly Ile Phe Asp Asp Gly His
 275 280 285 290
 Gly Ser Arg Gly Arg Glu Val Cys Arg Arg His Glu Leu Tyr Val Ser
 295 300 305
 Phe Arg Asp Leu Gly Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr
 310 315 320
 Ser Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asp Ser Cys
 325 330 335
 Met Asn Ala Thr Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met
 340 345 350
 Lys Pro Asp Val Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser
 355 360 365 370
 Ala Thr Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg
 375 380 385
 Lys His Arg Asn Met Val Val Lys Ala Cys Gly Cys His
 390 395

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1369 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1368
 (D) OTHER INFORMATION: /STANDARD NAME="60A"
- (x) PUBLICATION INFORMATION:
 (A) AUTHORS: WHARTON, KRISTI A.; THOMSEN, GERALD H.;
 GELBERT, WILLIAM M.
 (B) TITLE: DROSOPHILA 60A GENE...
 (C) JOURNAL: PROC. NAT'L ACAD. SCI. USA
 (D) VOLUME: 88
 (E) RELEVANT RESIDUES IN SEQ ID NO:3: FROM 1 TO 1368
 (F) PAGES: 9214-9218
 (G) DATE: OCT - 1991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATG TCG GGA CTG CGA AAC ACC TCG GAG GCC GTT GCA GTG CTC GCC TCC	48
Met Ser Gly Leu Arg Asn Thr Ser Glu Ala Val Ala Val Leu Ala Ser	
1 5 10 15	
CTG GGA CTC GGA ATG GTT CTG CTC ATG TTC GTG GCG ACC ACG CCG CCG	96
Leu Gly Leu Gly Met Val Leu Leu Met Phe Val Ala Thr Thr Pro Pro	
20 25 30	
GCC GTT GAG GCC ACC CAG TCG GGG ATT TAC ATA GAC AAC GGC AAG GAC	144
Ala Val Glu Ala Thr Gln Ser Gly Ile Tyr Ile Asp Asn Gly Lys Asp	
35 40 45	
CAG ACG ATC ATG CAC AGA GTG CTG AGC GAG GAC GAC AAG CTG GAC GTC	192
Gln Thr Ile Met His Arg Val Leu Ser Glu Asp Asp Lys Leu Asp Val	
50 55 60	
TCG TAC GAG ATC CTC GAG TTC CTG GGC ATC GCC GAA CGG CCG ACG CAC	240
Ser Tyr Glu Ile Leu Glu Phe Leu Gly Ile Ala Glu Arg Pro Thr His	
65 70 75 80	
CTG AGC AGC CAC CAG TTG TCG CTG AGG AAG TCG GCT CCC AAG TTC CTG	288
Leu Ser Ser His Gln Leu Ser Leu Arg Lys Ser Ala Pro Lys Phe Leu	
85 90 95	

CTG	GAC	GTC	TAC	CAC	CGC	ATC	ACG	GCG	GAG	GAG	GGT	CTC	AGC	GAT	CAG	336
Leu	Asp	Val	Tyr	His	Arg	Ile	Thr	Ala	Glu	Glu	Gly	Leu	Ser	Asp	Gln	
			100					105					110			
GAT	GAG	GAC	GAC	GAC	TAC	GAA	CGC	GGC	CAT	CGG	TCC	AGG	AGG	AGC	GCC	384
Asp	Glu	Asp	Asp	Asp	Tyr	Glu	Arg	Gly	His	Arg	Ser	Arg	Arg	Ser	Ala	
		115					120					125				
GAC	CTC	GAG	GAG	GAT	GAG	GGC	GAG	CAG	CAG	AAG	AAC	TTC	ATC	ACC	GAC	432
Asp	Leu	Glu	Glu	Asp	Glu	Gly	Glu	Gln	Gln	Lys	Asn	Phe	Ile	Thr	Asp	
	130					135					140					
CTG	GAC	AAG	CGG	GCC	ATC	GAC	GAG	AGC	GAC	ATC	ATC	ATG	ACC	TTC	CTG	480
Leu	Asp	Lys	Arg	Ala	Ile	Asp	Glu	Ser	Asp	Ile	Ile	Met	Thr	Phe	Leu	
145					150					155					160	
AAC	AAG	CGC	CAC	CAC	AAT	GTG	GAC	GAA	CTG	CGT	CAC	GAG	CAC	GGC	CGT	528
Asn	Lys	Arg	His	His	Asn	Val	Asp	Glu	Leu	Arg	His	Glu	His	Gly	Arg	
			165						170					175		
CGC	CTG	TGG	TTC	GAC	GTC	TCC	AAC	GTG	CCC	AAC	GAC	AAC	TAC	CTG	GTG	576
Arg	Leu	Trp	Phe	Asp	Val	Ser	Asn	Val	Pro	Asn	Asp	Asn	Tyr	Leu	Val	
			180					185					190			
ATG	GCC	GAG	CTG	CGC	ATC	TAT	CAG	AAC	GCC	AAC	GAG	GGC	AAG	TGG	CTG	624
Met	Ala	Glu	Leu	Arg	Ile	Tyr	Gln	Asn	Ala	Asn	Glu	Gly	Lys	Trp	Leu	
		195					200					205				
ACC	GCC	AAC	AGG	GAG	TTC	ACC	ATC	ACG	GTA	TAC	GCC	ATT	GGC	ACC	GGC	672
Thr	Ala	Asn	Arg	Glu	Phe	Thr	Ile	Thr	Val	Tyr	Ala	Ile	Gly	Thr	Gly	
	210					215					220					
ACG	CTG	GGC	CAG	CAC	ACC	ATG	GAG	CCG	CTG	TCC	TCG	GTG	AAC	ACC	ACC	720
Thr	Leu	Gly	Gln	His	Thr	Met	Glu	Pro	Leu	Ser	Ser	Val	Asn	Thr	Thr	
225					230					235					240	
GGG	GAC	TAC	GTG	GGC	TGG	TTG	GAG	CTC	AAC	GTG	ACC	GAG	GGC	CTG	CAC	768
Gly	Asp	Tyr	Val	Gly	Trp	Leu	Glu	Leu	Asn	Val	Thr	Glu	Gly	Leu	His	
			245						250					255		
GAG	TGG	CTG	GTC	AAG	TCG	AAG	GAC	AAT	CAT	GGC	ATC	TAC	ATT	GGA	GCA	816
Glu	Trp	Leu	Val	Lys	Ser	Lys	Asp	Asn	His	Gly	Ile	Tyr	Ile	Gly	Ala	
			260					265					270			
CAC	GCT	GTC	AAC	CGA	CCC	GAC	CGC	GAG	GTG	AAG	CTG	GAC	GAC	ATT	GGA	864
His	Ala	Val	Asn	Arg	Pro	Asp	Arg	Glu	Val	Lys	Leu	Asp	Asp	Ile	Gly	
		275					280					285				
CTG	ATC	CAC	CGC	AAG	GTG	GAC	GAC	GAG	TTC	CAG	CCC	TTC	ATG	ATC	GGC	912
Leu	Ile	His	Arg	Lys	Val	Asp	Asp	Glu	Phe	Gln	Pro	Phe	Met	Ile	Gly	
	290					295					300					

TTC	TTC	CGC	GGA	CCG	GAG	CTG	ATC	AAG	GCG	ACG	GCC	CAC	AGC	AGC	CAC	960
Phe	Phe	Arg	Gly	Pro	Glu	Leu	Ile	Lys	Ala	Thr	Ala	His	Ser	Ser	His	
305					310					315					320	
CAC	AGG	AGC	AAG	CGA	AGC	GCC	AGC	CAT	CCA	CGC	AAG	CGC	AAG	AAG	TCG	1008
His	Arg	Ser	Lys	Arg	Ser	Ala	Ser	His	Pro	Arg	Lys	Arg	Lys	Lys	Ser	
				325					330					335		
GTG	TCG	CCC	AAC	AAC	GTG	CCG	CTG	CTG	GAA	CCG	ATG	GAG	AGC	ACG	CGC	1056
Val	Ser	Pro	Asn	Asn	Val	Pro	Leu	Leu	Glu	Pro	Met	Glu	Ser	Thr	Arg	
			340					345					350			
AGC	TGC	CAG	ATG	CAG	ACC	CTG	TAC	ATA	GAC	TTC	AAG	GAT	CTG	GGC	TGG	1104
Ser	Cys	Gln	Met	Gln	Thr	Leu	Tyr	Ile	Asp	Phe	Lys	Asp	Leu	Gly	Trp	
		355					360					365				
CAT	GAC	TGG	ATC	ATC	GCA	CCA	GAG	GGC	TAT	GGC	GCC	TTC	TAC	TGC	AGC	1152
His	Asp	Trp	Ile	Ile	Ala	Pro	Glu	Gly	Tyr	Gly	Ala	Phe	Tyr	Cys	Ser	
	370					375					380					
GGC	GAG	TGC	AAT	TTC	CCG	CTC	AAT	GCG	CAC	ATG	AAC	GCC	ACG	AAC	CAT	1200
Gly	Glu	Cys	Asn	Phe	Pro	Leu	Asn	Ala	His	Met	Asn	Ala	Thr	Asn	His	
385					390					395					400	
GCG	ATC	GTC	CAG	ACC	CTG	GTC	CAC	CTG	CTG	GAG	CCC	AAG	AAG	GTG	CCC	1248
Ala	Ile	Val	Gln	Thr	Leu	Val	His	Leu	Leu	Glu	Pro	Lys	Lys	Val	Pro	
				405					410					415		
AAG	CCC	TGC	TGC	GCT	CCG	ACC	AGG	CTG	GGA	GCA	CTA	CCC	GTT	CTG	TAC	1296
Lys	Pro	Cys	Cys	Ala	Pro	Thr	Arg	Leu	Gly	Ala	Leu	Pro	Val	Leu	Tyr	
			420					425					430			
CAC	CTG	AAC	GAC	GAG	AAT	GTG	AAC	CTG	AAA	AAG	TAT	AGA	AAC	ATG	ATT	1344
His	Leu	Asn	Asp	Glu	Asn	Val	Asn	Leu	Lys	Lys	Tyr	Arg	Asn	Met	Ile	
		435					440					445				
GTG	AAA	TCC	TGC	GGG	TGC	CAT	TGA									1368
Val	Lys	Ser	Cys	Gly	Cys	His										
	450					455										

22 35
 22 35
 22 35

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```

Met Ser Gly Leu Arg Asn Thr Ser Glu Ala Val Ala Val Leu Ala Ser
 1           5           10           15
Leu Gly Leu Gly Met Val Leu Leu Met Phe Val Ala Thr Thr Pro Pro
      20           25           30
Ala Val Glu Ala Thr Gln Ser Gly Ile Tyr Ile Asp Asn Gly Lys Asp
      35           40           45
Gln Thr Ile Met His Arg Val Leu Ser Glu Asp Asp Lys Leu Asp Val
      50           55           60
Ser Tyr Glu Ile Leu Glu Phe Leu Gly Ile Ala Glu Arg Pro Thr His
      65           70           75           80
Leu Ser Ser His Gln Leu Ser Leu Arg Lys Ser Ala Pro Lys Phe Leu
      85           90           95
Leu Asp Val Tyr His Arg Ile Thr Ala Glu Glu Gly Leu Ser Asp Gln
      100          105          110
Asp Glu Asp Asp Asp Tyr Glu Arg Gly His Arg Ser Arg Arg Ser Ala
      115          120          125
Asp Leu Glu Glu Asp Glu Gly Glu Gln Gln Lys Asn Phe Ile Thr Asp
      130          135          140
Leu Asp Lys Arg Ala Ile Asp Glu Ser Asp Ile Ile Met Thr Phe Leu
      145          150          155          160
Asn Lys Arg His His Asn Val Asp Glu Leu Arg His Glu His Gly Arg
      165          170          175
Arg Leu Trp Phe Asp Val Ser Asn Val Pro Asn Asp Asn Tyr Leu Val
      180          185          190
Met Ala Glu Leu Arg Ile Tyr Gln Asn Ala Asn Glu Gly Lys Trp Leu
      195          200          205
Thr Ala Asn Arg Glu Phe Thr Ile Thr Val Tyr Ala Ile Gly Thr Gly
      210          215          220

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Thr Leu Gly Gln His Thr Met Glu Pro Leu Ser Ser Val Asn Thr Thr
 225 230 235 240
 Gly Asp Tyr Val Gly Trp Leu Glu Leu Asn Val Thr Glu Gly Leu His
 245 250 255
 Glu Trp Leu Val Lys Ser Lys Asp Asn His Gly Ile Tyr Ile Gly Ala
 260 265 270
 His Ala Val Asn Arg Pro Asp Arg Glu Val Lys Leu Asp Asp Ile Gly
 275 280 285
 Leu Ile His Arg Lys Val Asp Asp Glu Phe Gln Pro Phe Met Ile Gly
 290 295 300
 Phe Phe Arg Gly Pro Glu Leu Ile Lys Ala Thr Ala His Ser Ser His
 305 310 315 320
 His Arg Ser Lys Arg Ser Ala Ser His Pro Arg Lys Arg Lys Lys Ser
 325 330 335
 Val Ser Pro Asn Asn Val Pro Leu Leu Glu Pro Met Glu Ser Thr Arg
 340 345 350
 Ser Cys Gln Met Gln Thr Leu Tyr Ile Asp Phe Lys Asp Leu Gly Trp
 355 360 365
 His Asp Trp Ile Ile Ala Pro Glu Gly Tyr Gly Ala Phe Tyr Cys Ser
 370 375 380
 Gly Glu Cys Asn Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His
 385 390 395 400
 Ala Ile Val Gln Thr Leu Val His Leu Leu Glu Pro Lys Lys Val Pro
 405 410 415
 Lys Pro Cys Cys Ala Pro Thr Arg Leu Gly Ala Leu Pro Val Leu Tyr
 420 425 430
 His Leu Asn Asp Glu Asn Val Asn Leu Lys Lys Tyr Arg Asn Met Ile
 435 440 445
 Val Lys Ser Cys Gly Cys His
 450 455

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo Sapiens
- (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..102
 - (D) OTHER INFORMATION: /note="BMP3"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 104 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (ix) FEATURE:
 - (A) NAME/KEY: Protein
 - (B) LOCATION: 1..104
 - (D) OTHER INFORMATION: /note="BMP3"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Cys	Ala	Arg	Arg	Tyr	Leu	Lys	Val	Asp	Phe	Ala	Asp	Ile	Gly	Trp	Ser	1	5	10	15
Glu	Trp	Ile	Ile	Ser	Pro	Lys	Ser	Phe	Asp	Ala	Tyr	Try	Cys	Ser	Gly	20	25	30	
Ala	Cys	Gln	Phe	Pro	Met	Pro	Lys	Ser	Leu	Lys	Pro	Ser	Asn	His	Ala	35	40	45	
Thr	Ile	Gln	Ser	Ile	Val	Ala	Arg	Ala	Val	Gly	Val	Val	Pro	Gly	Ile	50	55	60	
Pro	Glu	Pro	Cys	Cys	Val	Pro	Glu	Lys	Met	Ser	Ser	Leu	Ser	Ile	Leu	65	70	75	80
Phe	Phe	Asp	Glu	Asn	Lys	Asn	Val	Val	Leu	Lys	Val	Tyr	Pro	Asn	Met	85	90	95	
Thr	Val	Glu	Ser	Cys	Ala	Cys	Arg									100			

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: HOMO SAPIENS

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: /note= "BMP5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Cys	Lys	Lys	His	Glu	Leu	Tyr	Val	Ser	Phe	Arg	Asp	Leu	Gly	Trp	Gln	1	5	10	15
Asp	Trp	Ile	Ile	Ala	Pro	Glu	Gly	Tyr	Ala	Ala	Phe	Tyr	Cys	Asp	Gly	20	25	30	
Glu	Cys	Ser	Phe	Pro	Leu	Asn	Ala	His	Met	Asn	Ala	Thr	Asn	His	Ala	35	40	45	
Ile	Val	Gln	Thr	Leu	Val	His	Leu	Met	Phe	Pro	Asp	His	Val	Pro	Lys	50	55	60	
Pro	Cys	Cys	Ala	Pro	Thr	Lys	Leu	Asn	Ala	Ile	Ser	Val	Leu	Tyr	Phe	65	70	75	80
Asp	Asp	Ser	Ser	Asn	Val	Ile	Leu	Lys	Lys	Tyr	Arg	Asn	Met	Val	Val	85	90	95	
Arg	Ser	Cys	Gly	Cys	His	100													

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: HOMO SAPIENS

(ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..102
 (D) OTHER INFORMATION: /note= "BMP6"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Cys	Arg	Lys	His	Glu	Leu	Tyr	Val	Ser	Phe	Gln	Asp	Leu	Gly	Trp	Gln	1	5	10	15
Asp	Trp	Ile	Ile	Ala	Pro	Lys	Gly	Tyr	Ala	Ala	Asn	Tyr	Cys	Asp	Gly	20	25	30	
Glu	Cys	Ser	Phe	Pro	Leu	Asn	Ala	His	Met	Asn	Ala	Thr	Asn	His	Ala	35	40	45	
Ile	Val	Gln	Thr	Leu	Val	His	Leu	Met	Asn	Pro	Glu	Tyr	Val	Pro	Lys	50	55	60	
Pro	Cys	Cys	Ala	Pro	Thr	Lys	Leu	Asn	Ala	Ile	Ser	Val	Leu	Tyr	Phe	65	70	75	80
Asp	Asp	Asn	Ser	Asn	Val	Ile	Leu	Lys	Lys	Tyr	Arg	Trp	Met	Val	Val	85	90	95	
Arg	Ala	Cys	Gly	Cys	His	100													

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein
 (B) LOCATION: 1..102
 (D) OTHER INFORMATION: /label= OPX
 /note= "WHEREIN XAA AT EACH POS'N IS INDEPENDENTLY
 SELECTED FROM THE RESIDUES OCCURRING AT THE
 CORRESPONDING POS'N IN THE C-TERMINAL SEQUENCE OF MOUSE
 OR HUMAN OP1 OR OP2 (SEE SEQ. ID NOS. 5,6,7 and 8 or
 16,18,20 and 22.)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```

Cys Xaa Xaa His Glu Leu Tyr Val Xaa Phe Xaa Asp Leu Gly Trp Xaa
1          5          10          15
Asp Trp Xaa Ile Ala Pro Xaa Gly Tyr Xaa Ala Tyr Tyr Cys Glu Gly
20          25          30
Glu Cys Xaa Phe Pro Leu Xaa Ser Xaa Met Asn Ala Thr Asn His Ala
35          40          45
Ile Xaa Gln Xaa Leu Val His Xaa Xaa Xaa Pro Xaa Xaa Val Pro Lys
50          55          60
Xaa Cys Cys Ala Pro Thr Xaa Leu Xaa Ala Xaa Ser Val Leu Tyr Xaa
65          70          75          80
Asp Xaa Ser Xaa Asn Val Xaa Leu Xaa Lys Xaa Arg Asn Met Val Val
85          90          95
Xaa Ala Cys Gly Cys His
100

```

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acids
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME: Generic Sequence 5
- (D) OTHER INFORMATION: wherein each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```

Leu Xaa Xaa Xaa Phe
   1           5
Xaa Xaa Xaa Gly Trp Xaa Xaa Trp Xaa
   10
Xaa Xaa Pro Xaa Xaa Xaa Xaa Ala
  15           20
Xaa Tyr Cys Xaa Gly Xaa Cys Xaa
  25           30
Xaa Pro Xaa Xaa Xaa Xaa Xaa
           35
Xaa Xaa Xaa Asn His Ala Xaa Xaa
  40           45
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
           50
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
  55           60
Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa
  65
Xaa Xaa Xaa Leu Xaa Xaa Xaa
  70           75
Xaa Xaa Xaa Xaa Val Xaa Leu Xaa
           80
Xaa Xaa Xaa Xaa Met Xaa Val Xaa
  85           90
Xaa Cys Xaa Cys Xaa
           95

```

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acids
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME: Generic Sequence 6
- (D) OTHER INFORMATION: wherein each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

```

Cys Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Phe
 1               5               10
Xaa Xaa Xaa Gly Trp Xaa Xaa Trp Xaa
              15
Xaa Xaa Pro Xaa Xaa Xaa Xaa Ala
 20               25
Xaa Tyr Cys Xaa Gly Xaa Cys Xaa
              30               35
Xaa Pro Xaa Xaa Xaa Xaa Xaa
              40
Xaa Xaa Xaa Asn His Ala Xaa Xaa
              45               50
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
              55
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
 60               65
Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa
              70
Xaa Xaa Xaa Leu Xaa Xaa Xaa
 75               80
Xaa Xaa Xaa Xaa Val Xaa Leu Xaa
              85
Xaa Xaa Xaa Xaa Met Xaa Val Xaa
 90               95
Xaa Cys Xaa Cys Xaa
              100

```

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1238 base pairs, 372 amino acids
 - (B) TYPE: nucleic acid, amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) ORIGINAL SOURCE:
 - (A) ORGANISM: human
 - (F) TISSUE TYPE: BRAIN
- (iv) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION:
 - (D) OTHER INFORMATION:
 - /product= "GDF-1"
 - /note= "GDF-1 CDNA"
- (x) PUBLICATION INFORMATION:
 - (A) AUTHORS: Lee, Se-Jin
 - (B) TITLE: Expression of Growth/Differentiation Factor 1
 - (C) JOURNAL: Proc. Nat'l Acad. Sci.
 - (D) VOLUME: 88
 - (E) RELEVANT RESIDUES: 1-1238
 - (F) PAGES: 4250-4254
 - (G) DATE: May-1991
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```

GGGGACACCG GCCCGCCCT CAGCCCACTG GTCCCGGGCC GCCGCGGACC CTGCGCACTC      60
TCTGGTCATC GCCTGGGAGG AAG ATG CCA CCG CCG CAG CAA GGT CCC TGC GGC      113
                Met Pro Pro Pro Gln Gln Gly Pro Cys Gly
                1                      5                      10

CAC CAC CTC CTC CTC CTC CTG GCC CTG CTG CTG CCC TCG CTG CCC      158
His His Leu Leu Leu Leu Leu Ala Leu Leu Leu Pro Ser Leu Pro
                15                      20                      25

CTG ACC CGC GCC CCC GTG CCC CCA GGC CCA GCC GCC GCC CTG CTC      203
Leu Thr Arg Ala Pro Val Pro Pro Gly Pro Ala Ala Ala Leu Leu
                30                      35                      40

CAG GCT CTA GGA CTG CGC GAT GAG CCC CAG GGT GCC CCC AGG CTC      248
Gln Ala Leu Gly Leu Arg Asp Glu Pro Gln Gly Ala Pro Arg Leu
                45                      50                      55

```

CGG	CCG	GTT	CCC	CCG	GTC	ATG	TGG	CGC	CTG	TTT	CGA	CGC	CGG	GAC	293
Arg	Pro	Val	Pro	Pro	Val	Met	Trp	Arg	Leu	Phe	Arg	Arg	Arg	Asp	
				60					65					70	
CCC	CAG	GAG	ACC	AGG	TCT	GGC	TCG	CGG	CGG	ACG	TCC	CCA	GGG	GTC	338
Pro	Gln	Glu	Thr	Arg	Ser	Gly	Ser	Arg	Arg	Thr	Ser	Pro	Gly	Val	
				75					80					85	
ACC	CTG	CAA	CCG	TGC	CAC	GTG	GAG	GAG	CTG	GGG	GTC	GCC	GGA	AAC	383
Thr	Leu	Gln	Pro	Cys	His	Val	Glu	Glu	Leu	Gly	Val	Ala	Gly	Asn	
				90					95					100	
ATC	GTG	CGC	CAC	ATC	CCG	GAC	CGC	GGT	GCG	CCC	ACC	CGG	GCC	TCG	428
Ile	Val	Arg	His	Ile	Pro	Asp	Arg	Gly	Ala	Pro	Thr	Arg	Ala	Ser	
				105					110					115	
GAG	CCT	GTC	TCG	GCC	GCG	GGG	CAT	TGC	CCT	GAG	TGG	ACA	GTC	GTC	473
Glu	Pro	Val	Ser	Ala	Ala	Gly	His	Cys	Pro	Glu	Trp	Thr	Val	Val	
				120					125					130	
TTC	GAC	CTG	TCG	GCT	GTG	GAA	CCC	GCT	GAG	CGC	CCG	AGC	CGG	GCC	518
Phe	Asp	Leu	Ser	Ala	Val	Glu	Pro	Ala	Glu	Arg	Pro	Ser	Arg	Ala	
				135					140					145	
CGC	CTG	GAG	CTG	CGT	TTC	GCG	GCG	GCG	GCG	GCG	GCA	GCC	CCG	GAG	563
Arg	Leu	Glu	Leu	Arg	Phe	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Pro	Glu	
				150					155					160	
GGC	GGC	TGG	GAG	CTG	AGC	GTG	GCG	CAA	GCG	GGC	CAG	GGC	GCG	GGC	608
Gly	Gly	Trp	Glu	Leu	Ser	Val	Ala	Gln	Ala	Gly	Gln	Gly	Ala	Gly	
				165					170					175	
GCG	GAC	CCC	GGG	CCG	GTG	CTG	CTC	CGC	CAG	TTG	GTG	CCC	GCC	CTG	653
Ala	Asp	Pro	Gly	Pro	Val	Leu	Leu	Arg	Gln	Leu	Val	Pro	Ala	Leu	
				180					185					190	
GGG	CCG	CCA	GTG	CGC	GCG	GAG	CTG	CTG	GGC	GCC	GCT	TGG	GCT	CGC	698
Gly	Pro	Pro	Val	Arg	Ala	Glu	Leu	Leu	Gly	Ala	Ala	Trp	Ala	Arg	
				195					200					205	
AAC	GCC	TCA	TGG	CCG	CGC	AGC	CTC	CGC	CTG	GCG	CTG	GCG	CTA	CGC	743
Asn	Ala	Ser	Trp	Pro	Arg	Ser	Leu	Arg	Leu	Ala	Leu	Ala	Leu	Arg	
				210					215					220	
CCC	CGG	GCC	CCT	GCC	GCC	TGC	GCG	CGC	CTG	GCC	GAG	GCC	TCG	CTG	788
Pro	Arg	Ala	Pro	Ala	Ala	Cys	Ala	Arg	Leu	Ala	Glu	Ala	Ser	Leu	
				225					230					235	
CTG	CTG	GTG	ACC	CTC	GAC	CCG	CGC	CTG	TGC	CAC	CCC	CTG	GCC	CGG	833
Leu	Leu	Val	Thr	Leu	Asp	Pro	Arg	Leu	Cys	His	Pro	Leu	Ala	Arg	
				240					245					250	

(34) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v1) ORIGINAL SOURCE:

- (A) ORGANISM: human
(F) TISSUE TYPE: BRAIN

(ix) **FEATURE:**

- ```
(A) NAME/KEY: CDS
(B) LOCATION:
(D) OTHER INFORMATION: /function=
 /product= "GDF-1"
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

[illegible]

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|-----|-----|
| Glu | Pro | Val | Ser | Ala | Ala | Gly | His | Cys | Pro | Glu | Trp | Thr | Val | Val |  | 120 | 125 | 130 |
| Phe | Asp | Leu | Ser | Ala | Val | Glu | Pro | Ala | Glu | Arg | Pro | Ser | Arg | Ala |  | 135 | 140 | 145 |
| Arg | Leu | Glu | Leu | Arg | Phe | Ala | Ala | Ala | Ala | Ala | Ala | Ala | Pro | Glu |  | 150 | 155 | 160 |
| Gly | Gly | Trp | Glu | Leu | Ser | Val | Ala | Gln | Ala | Gly | Gln | Gly | Ala | Gly |  | 165 | 170 | 175 |
| Ala | Asp | Pro | Gly | Pro | Val | Leu | Leu | Arg | Gln | Leu | Val | Pro | Ala | Leu |  | 180 | 185 | 190 |
| Gly | Pro | Pro | Val | Arg | Ala | Glu | Leu | Leu | Gly | Ala | Ala | Trp | Ala | Arg |  | 195 | 200 | 205 |
| Asn | Ala | Ser | Trp | Pro | Arg | Ser | Leu | Arg | Leu | Ala | Leu | Ala | Leu | Arg |  | 210 | 215 | 220 |
| Pro | Arg | Ala | Pro | Ala | Ala | Cys | Ala | Arg | Leu | Ala | Glu | Ala | Ser | Leu |  | 225 | 230 | 235 |
| Leu | Leu | Val | Thr | Leu | Asp | Pro | Arg | Leu | Cys | His | Pro | Leu | Ala | Arg |  | 240 | 245 | 250 |
| Pro | Arg | Arg | Asp | Ala | Glu | Pro | Val | Leu | Gly | Gly | Gly | Pro | Gly | Gly |  | 255 | 260 | 265 |
| Ala | Cys | Arg | Ala | Arg | Arg | Leu | Tyr | Val | Ser | Phe | Arg | Glu | Val | Gly |  | 270 | 275 | 280 |
| Trp | His | Arg | Trp | Val | Ile | Arg | Pro | Arg | Gly | Phe | Leu | Ala | Asn | Tyr |  | 285 | 290 | 295 |
| Cys | Gln | Gly | Gln | Cys | Ala | Leu | Pro | Val | Ala | Leu | Ser | Gly | Ser | Gly |  | 300 | 305 | 310 |
| Gly | Pro | Pro | Ala | Leu | Asn | His | Ala | Val | Leu | Arg | Ala | Leu | Met | His |  | 315 | 320 | 325 |
| Ala | Ala | Ala | Pro | Gly | Ala | Ala | Asp | Leu | Pro | Cys | Cys | Val | Pro | Ala |  | 330 | 335 | 340 |
| Arg | Leu | Ser | Pro | Ile | Ser | Val | Leu | Phe | Phe | Asp | Asn | Ser | Asp | Asn |  | 345 | 350 | 355 |
| Val | Val | Leu | Arg | Gln | Tyr | Glu | Asp | Met | Val | Val | Asp | Glu | Cys | Gly |  | 360 | 365 | 370 |
| Cys | Arg |     |     |     |     |     |     |     |     |     |     |     |     |     |  | 372 |     |     |

What is claimed is:

1. A method of screening candidate compounds for the ability to modulate the effective concentration of a morphogen in an organism, said method comprising  
incubating a candidate compound with cells from a test tissue type known to produce a morphogen for a time sufficient to allow said compound to affect the production of said morphogen, and  
assaying said cells for a parameter indicative of a change in the level of production of said morphogen.
2. The method of claim 1 wherein said morphogen is OP-1.
3. The method of claim 2 wherein said test tissue type is a human renal-derived tissue.
4. The method of claim 3 wherein said renal-derived tissue is a kidney or bladder-derived tissue.
5. The method of claim 2 wherein said test tissue type is adrenal-derived tissue.
6. The method of claim 1 wherein said morphogen is GDF-1.
7. The method of claim 6 wherein said test tissue type is derived from human nerve tissue.

8. The method of claim 7 wherein said nerve tissue is brain-derived tissue.

9. The method of claim 1 wherein said morphogen is DPP.

10. The method of claim 9 wherein said test tissue type is derived from one of the following drosophila tissues: dorsal ectoderm, epithelial imaginal disc visceral mesoderm, or gut endoderm.

11. The method of claim 1 wherein said morphogen is Vgr-1.

12. The method of claim 11 wherein said test tissue type is mouse lung tissue.

13. The method of claim 1 wherein said morphogen is Vgl.

14. The method of claim 13 wherein said test tissue type is xenopus fetal endoderm tissue.

15. A method of assessing a tissue of an organism for its level of production of a morphogen and for screening candidate compounds for the ability to modulate the effective concentration of said morphogen produced by cells of said tissue, said method comprising  
selecting a test tissue type producing a high level of morphogen relative to the level of morphogen produced by other tissue types;

incubating a candidate compound with cultured cells of said selected tissue type for a time sufficient to allow said compound to affect the production of said morphogen; and

assaying said selected tissue cells for a parameter indicative of a change in the level of production of said morphogen.

16. The method of claim 1 or 15 wherein said parameter indicative of the level of said morphogen is determined using an antibody specific for said morphogen.

17. The method of claim 1 or 15 wherein said parameter indicative of the level of said morphogen is determined by measuring cellular proliferation in cells which are sensitive to the concentration of secreted OP-1.

18. The method of claim 1 or 15 wherein said parameter indicative of the level of said morphogen is determined using a nucleic acid probe that hybridizes under stringent conditions with nucleic acid encoding said morphogen.

19. The method of claim 18 wherein said morphogen comprises a minimally active core C-terminal region comprising at least six cysteine residues, and said nucleic acid probe hybridizes with an mRNA encoding a region N-terminal to said core region.

20. The method of claim 18 wherein said morphogen comprises a minimally active core C-terminal region

comprising at least six cysteine residues, and said nucleic acid probe hybridizes with an mRNA encoding a region 3' to said core region.

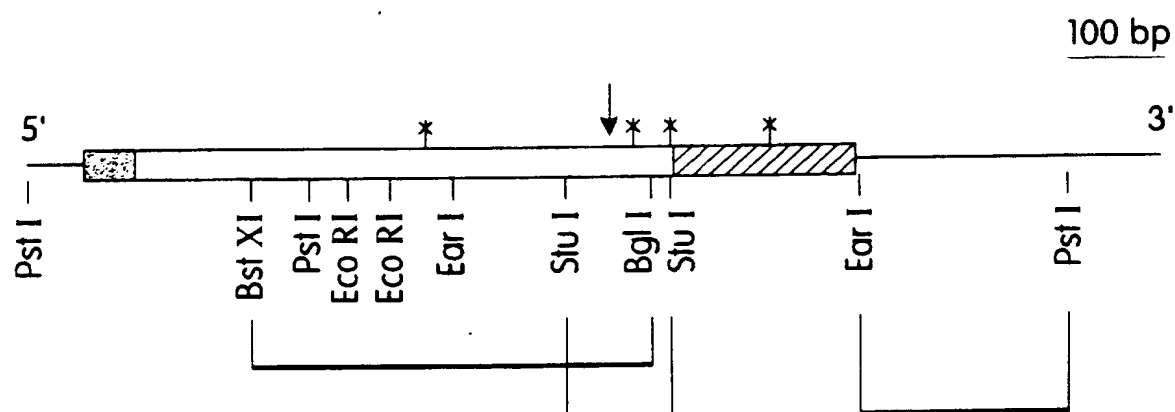


Fig. 1

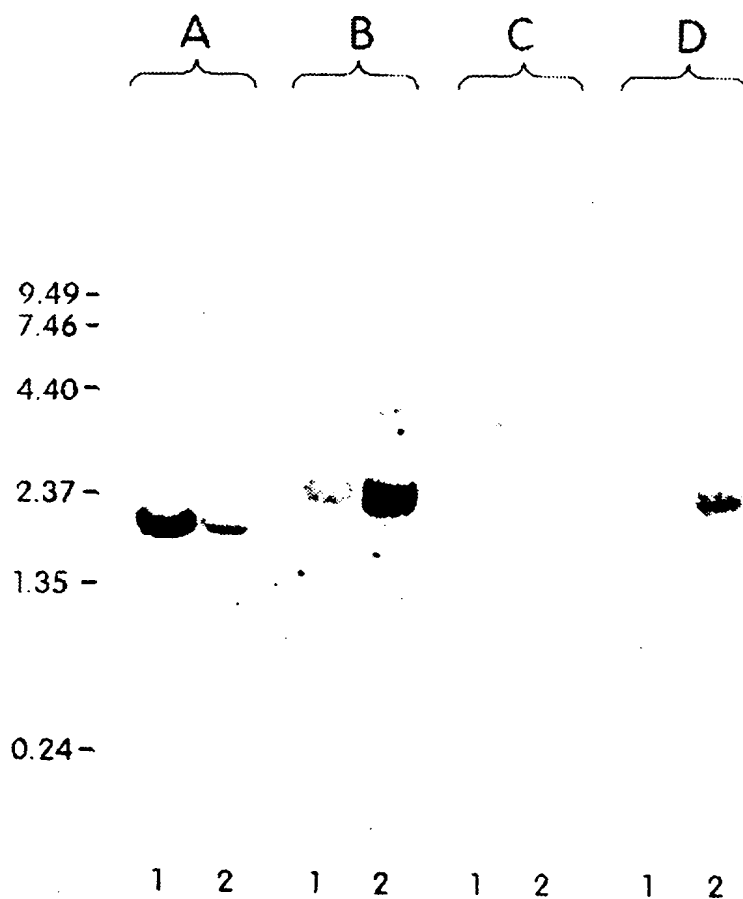


Fig. 2

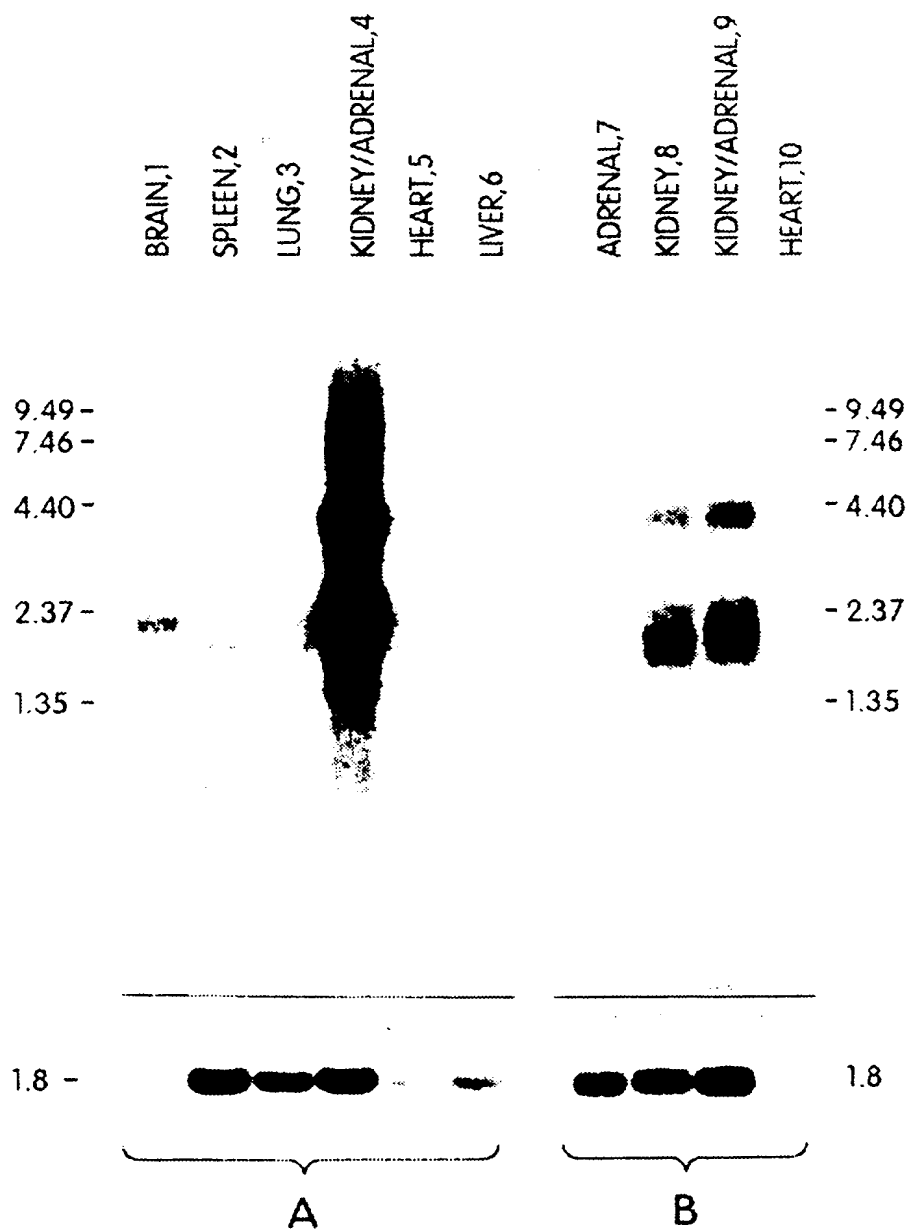


Fig. 3

## International Application No.

|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                                                                                                                                                   |                                                     |
|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------|
| <b>I. CLASSIFICATION OF SUBJECT MATTER</b> (if several classification symbols apply, indicate all) <sup>6</sup><br>According to International Patent Classification (IPC) or to both National Classification and IPC<br>Int.Cl. 5 C12Q1/02; G01N33/68                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |                                                                                                                                                                                                   |                                                     |
| <b>II. FIELDS SEARCHED</b><br>Minimum Documentation Searched <sup>7</sup>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                                                                                                                                                   |                                                     |
| Classification System                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Classification Symbols                                                                                                                                                                            |                                                     |
| Int.Cl. 5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | C12Q ; G01N ; C07K                                                                                                                                                                                |                                                     |
| Documentation Searched other than Minimum Documentation<br>to the extent that such Documents are included in the Fields Searched <sup>8</sup>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |                                                                                                                                                                                                   |                                                     |
| <b>III. DOCUMENTS CONSIDERED TO BE RELEVANT<sup>9</sup></b>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |                                                                                                                                                                                                   |                                                     |
| Category <sup>9</sup>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Citation of Document, <sup>11</sup> with indication, where appropriate, of the relevant passages <sup>12</sup>                                                                                    | Relevant to Claim No. <sup>13</sup>                 |
| X                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | JOURNAL OF BONE AND MINERAL RESEARCH<br>vol. 6, no. 7, July 1991,<br>pages 767 - 777<br>H.ZHOU ET AL.                                                                                             | 1, 15, 18                                           |
| Y                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | see abstract<br>see page 768, left column, line 22 - line 55<br>see page 771, right column, line 12 - page 772, left column, line 8<br>see page 774, right column, line 4 - line 44<br>---<br>-/- | 6                                                   |
| <sup>9</sup> Special categories of cited documents: <sup>10</sup><br><sup>"A"</sup> document defining the general state of the art which is not considered to be of particular relevance<br><sup>"E"</sup> earlier document but published on or after the international filing date<br><sup>"L"</sup> document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)<br><sup>"O"</sup> document referring to an oral disclosure, use, exhibition or other means<br><sup>"P"</sup> document published prior to the international filing date but later than the priority date claimed<br><sup>"T"</sup> later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention<br><sup>"X"</sup> document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step<br><sup>"Y"</sup> document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.<br><sup>"A"</sup> document member of the same patent family |                                                                                                                                                                                                   |                                                     |
| <b>IV. CERTIFICATION</b>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |                                                                                                                                                                                                   |                                                     |
| Date of the Actual Completion of the International Search                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                                                                                                                                                   | Date of Mailing of this International Search Report |
| 09 DECEMBER 1992                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |                                                                                                                                                                                                   | 13. 01. 93                                          |
| International Searching Authority<br>EUROPEAN PATENT OFFICE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |                                                                                                                                                                                                   | Signature of Authorized Officer<br>LUZZATTO E.R.    |

| III. DOCUMENTS CONSIDERED TO BE RELEVANT (CONTINUED FROM THE SECOND SHEET) |                                                                                                                                                                                                                                                                               |                       |
|----------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------|
| Category *                                                                 | Citation of Document, with indication, where appropriate, of the relevant passages                                                                                                                                                                                            | Relevant to Claim No. |
| X                                                                          | <p>PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA.<br/>vol. 86, June 1989, WASHINGTON US<br/>pages 4554 - 4558<br/>K.LYONS ET AL.<br/>cited in the application<br/>see abstract<br/>see page 4557, left column, line 34 - page 4558, line 18; figure 5</p> <p>---</p> | 1, 11, 15, 19         |
| X                                                                          | <p>WO,A,9 102 744 (CELTRIX LABORATORIES)<br/>7 March 1991<br/>see page 1, line 1 - page 3, line 34<br/>see page 29, line 1 - line 28</p> <p>---</p>                                                                                                                           | 15, 16                |
| Y                                                                          | <p>PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA.<br/>vol. 88, May 1991, WASHINGTON US<br/>pages 4250 - 4254<br/>S.-J. LEE<br/>see abstract</p> <p>---</p>                                                                                                           | 6                     |
| Y                                                                          | <p>WO,A,9 000 619 (UNIVERSITY COLLEGE LONDON)<br/>25 January 1990<br/>see page 1, line 1 - page 2, line 18<br/>see page 4, line 14 - page 14, line 10</p> <p>---</p>                                                                                                          | 1, 15                 |
| P,Y                                                                        | <p>BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS.<br/>vol. 179, no. 1, 30 August 1991, DULUTH, MINNESOTA US<br/>pages 116 - 123<br/>E. ÖZKAYANAK ET AL.<br/>see the whole document</p> <p>-----</p>                                                                     | 1, 15                 |

**ANNEX TO THE INTERNATIONAL SEARCH REPORT  
ON INTERNATIONAL PATENT APPLICATION NO.**

US 9207359  
SA 64596

This annex lists the patent family members relating to the patent documents cited in the above-mentioned international search report. The members are as contained in the European Patent Office EDP file on  
The European Patent Office is in no way liable for these particulars which are merely given for the purpose of information. 09/12/92

| Patent document<br>cited in search report | Publication<br>date | Patent family<br>member(s) | Publication<br>date |
|-------------------------------------------|---------------------|----------------------------|---------------------|
| WO-A-9102744                              | 07-03-91            | AU-A- 6187090              | 03-04-91            |
|                                           |                     | CA-A- 2064878              | 22-02-91            |
|                                           |                     | EP-A- 0489062              | 10-06-92            |
| -----                                     |                     |                            |                     |
| WO-A-9000619                              | 25-01-90            | JP-T- 3505669              | 12-12-91            |
| -----                                     |                     |                            |                     |